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 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

**If more than one search is submitted, please prioritize searches in order of need.**

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

\*\*\*\*\*  
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Searcher: \_\_\_\_\_

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Clerical Prep Time: 10

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**Type of Search**

NA Sequence (#) 2

AA Sequence (#) 2

Structure (#) \_\_\_\_\_

Bibliographic \_\_\_\_\_

Litigation \_\_\_\_\_

Fulltext \_\_\_\_\_

Patent Family \_\_\_\_\_

Other \_\_\_\_\_

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PubMed ?

Other Formats:  Links: ☐ Order this document*Oncogene* 1999 Jan 14;18(2):559-64

## A tumor specific single chain antibody dependent gene expression system.

Mary MN, Venot C, Caron de Fromentel C, Debussche L, Conseiller E, Cochet O, Gruel N, Teillaud JL, Schweighoffer F, Tocque B, Bracco L

Gene Medicine Department, Rhone-Poulenc Rorer S.A., Vitry-sur-Seine, France.

The design of conditional gene expression systems restricted to given tissues or cellular types is an important issue of gene therapy. Systems based on the targeting of molecules characteristic of the pathological state of tissues would be of interest. We have developed a synthetic transcription factor by fusing a single chain antibody (scFv) directed against p53 with the bacterial tetracycline repressor as a DNA binding domain. This hybrid protein binds to p53 and can interact with a synthetic promoter containing tetracycline-operator sequences. Gene expression can now be specifically achieved in tumor cells harboring an endogenous mutant p53 but not in a wild-type p53 containing tumor cell line or in a non-transformed cell line. Thus, a functional transactivator centered on single chain antibodies can be expressed intracellularly and induce gene expression in a scFv-mediated specific manner. This novel class of transcriptional transactivators could be referred as 'trabodies' for transcription-activating-antibodies. The trabodies technology could be useful to any cell type in which a disease related protein could be the target of specific antibodies.

PMID: 9927213, UI: 99124403

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*Oncogene* 1999 Jan 14;18(2):551-7

## Restoration of transcriptional activity of p53 mutants in human tumour cells by intracellular expression of anti-p53 single chain Fv fragments.

Caron de Fromental C, Gruel N, Venot C, Debussche L, Conseiller E, Dureuil C, Teillaud JL, Tocque B, Bracco L

Gene Medicine Department, Rhone-Poulenc Rorer SA, Vitry sur Seine, France.

We report here the production and the properties of single chain Fv fragments (scFvs) derived from the anti-p53 monoclonal antibodies PAb421 and 11D3. 11D3 is a newly generated monoclonal antibody which exhibits properties very comparable to those of PAb421. The scFvs PAb421 and 11D3 are able to stably associate with p53 and to restore the DNA binding activity of some p53 mutants in vitro. When expressed in p53 -/-human tumour cells, the scFv421 is essentially localized in the cytoplasm in the absence of p53, and in the nucleus when exogenous p53 is present. Thus, p53 is also able to stably associate with an anti-p53 scFv in cells. Cotransfection of p53 -/- human tumour cells with expression vectors encoding the His273 p53 mutant and either scFv leads to restoration of the p53 mutant deficient transcriptional activity. These data demonstrate that, in human tumour cells, these scFvs are able to restore a function essential for the tumour suppressor activity of p53 and may represent a novel class of molecules for p53-based cancer therapy.

PMID: 9927212, UI: 99124402

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Other Formats:  Links:   ☐ Order this document*Biochem Biophys Res Commun* 1997 Jan 13;230(2):242-6

## Characterization of scFv-421, a single-chain antibody targeted to p53.

Jannot CB, Hynes NE

Friedrich Miescher Institute, Basel, Switzerland.

A gene encoding a single-chain antibody (scFv) which specifically binds the tumor suppressor protein p53 has been constructed from RNA of hybridoma cells producing Pab 421. scFv-421 which was expressed and purified from bacteria specifically binds p53. scFv-421, as well as the previously described scFv-FRP5 and -R1R (1), were expressed intracellularly in mammalian cells and targeted to different subcellular locations, including the nucleus, cytoplasm, and endoplasmic reticulum (ER). High levels of all ER targeted scFv proteins, but not nuclear or cytoplasmic targeted proteins, were found in transfected COS-1 cells. In an attempt to stabilize the proteins, sequences encoding the mouse immunoglobulin CK constant domain were added to each scFv construct. This led to a moderate increase in the cytoplasmic expression of scFv-FRP5.

PMID: 9016757, UI: 97168950

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PubMed

PubMed QUERY

Other Formats:  Links: ☐ Order this document*Oncogene* 1998 Nov 12;17(19):2445-56

## Characterization of a new intrabody directed against the N-terminal region of human p53.

Cohen PA, Mani JC, Lane DP

Department of Biochemistry, Medical Sciences Institute, University of Dundee, UK.

Genes encoding the rearranged immunoglobulin heavy and light chain variable regions of DO-1, a monoclonal antibody directed against human p53, have been used to construct a single-chain antibody. DO-1 recognizes an N-terminal epitope in the region involved in the transactivation function of p53 and the binding of Mdm2. The DO-1 single chain scFv expressed in the periplasm of *E. coli* or at the surface of the filamentous phage M13 retained the immunological specificity and affinity of the full length antibody. Furthermore, the DO-1 recombinant antibody was able to inhibit the in vitro binding of Hdm2, and was shown to be a powerful protecting agent of p53's DNA binding activity at 37 degrees C. The DO-1 single-chain antibody has been used to construct single-chain intracellular antibodies (intrabodies) for expression in the cytoplasm and the nucleus of mammalian cells. These anti-p53 intrabodies were additionally modified by addition of a Ckappa domain to increase cytoplasmic and nuclear stability. Here we show that expression of the DO-1 single-chain antibody in the H1299 cell line results in an inhibition of p53's transactivation function. The DO-1 intrabody is a useful tool to study those functions of p53 driven by the N-terminal region of the protein.

PMID: 9824155, UI: 99039761

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OM protein - protein search, using sw model

Run on: February 12, 2001, 15:23:21 ; Search time 28.25 Seconds

(without alignments)  
301.390 Million cell updates/sec

Title: US-09-297-181-4

Perfect score: 1335

Sequence: 1 QVKLOESCAELVRSQASVNL.....YCKQSYNLPFGGKLEIK 249

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing First 45 summaries

Database :

A.Geneseq\_36.\*  
1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SIDSL/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SIDSL/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SIDSL/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1315	100.0	249	19 W60770	Single chain antib
2	1024.5	77.9	288	20 W82743	Fusion protein p53
3	1024.5	77.9	673	20 W82742	Plasmodium p53
4	961	73.1	243	19 W60769	Single chain antih
5	955	72.6	535	18 W28491	Human p53 protein
6	955	72.6	535	18 W28492	Human p53 protein
7	951	72.3	580	20 W90217	Bispecific tetra
8	942	71.6	556	20 W90218	Bispecific tetra
9	932.5	70.9	437	19 W37738	Nucleotide sequenc
10	930	70.0	248	20 Y17960	Mouse scfv fragmen
11	921	70.0	248	20 Y17964	Mouse scfv fragmen
12	906	68.9	281	20 W82744	Fusion protein p1c

13	906	68.9	666	20 W82745	Fusion protein (80
14	901	68.5	248	20 Y17965	Mouse scfv fragmen
15	883	67.1	270	16 R75719	MpF-23 antibody
16	880	66.9	268	20 W90222	Anti-B7.2 monosp
17	877.5	66.7	282	18 W35564	HindIII-EcoRI Inse
18	877.5	66.7	282	18 W09818	VH4715-linker-VL47
19	877	66.7	553	18 W11508	Single chain anti-
20	877	66.7	553	20 W73223	H22-anti-CEA antib
21	868.5	66.0	532	18 W35565	HindIII-EcoRI Inse
22	850	64.6	248	19 W58826	Human CD30 binding
23	849.5	64.6	263	20 W90226	Anti-B7.2 monosp
24	846	64.3	248	19 W63830	Transformant CDM/1
25	842.5	64.1	241	20 Y21882	Amino acid sequenc
26	831.5	63.2	277	14 R39336	scfv fragment enco
27	830	63.1	269	16 R76682	Human ONS-M21 anti
28	830	63.1	269	17 W04397	Chimaeric human/mu
29	828	63.0	238	20 Y21880	Amino acid sequenc
30	823.5	62.6	244	16 R79867	Anti-BGFR single c
31	818	62.2	301	18 W11507	Single chain, huma
32	818	62.2	301	20 W73217	Multispecific sing
33	816.5	62.1	242	16 R79872	Anti-BGFR single c
34	814.5	61.9	244	16 R79873	Anti-BGFR single c
35	814	61.9	273	20 W90224	Anti-B7.1/anti-B7.
36	813.5	61.9	242	16 R79870	Anti-BGFR single c
37	811.5	61.7	246	16 R79869	Anti-BGFR single c
38	809.5	61.6	249	9 P80154	Biosynthetic antib
39	808.5	61.5	244	16 R79868	Anti-BGFR single c
40	807.5	61.4	482	20 Y06915	Amino acid sequenc
41	805	61.2	242	20 Y17961	Mouse scfv fragmen
42	803.5	61.1	483	20 W80099	A protein comprisi
43	803.5	61.1	483	21 Y57254	Divalent CC49/212
44	803.5	61.1	483	21 Y80924	Bivalent single ch
45	803.5	61.1	486	14 R37649	Sequence of divale

#### ALIGNMENTS

RESULT 1  
W60770  
ID W60770 standard; Protein: 249 AA.  
XX  
AC W60770;  
XX  
DT 08-SEP-1998 (first entry)  
XX  
DE Single chain antibody (scfv) D3M that binds to mutant p53 proteins.  
XX  
XX Single chain antibody; scfv D3M; mouse; p53 protein; oligomerisation;  
KW regulatory domain; p53 mutant; H273; W248; G281;  
KW p53-dependent trans-activating activity; restoration;  
KW tumour-suppressing activity; tumour cell; treatment;  
KW hyper-proliferation; cancer; re-stenosis; ss.  
XX  
OS Mus sp.  
XX  
PN W09818825-A1.  
XX  
PD 07-MAY-1998.  
XX  
PF 27-OCT-1997; 97WO-FR01921.  
XX  
PR 29-OCT-1996; 96FR-0013176.  
XX  
PA (RHON ) RHONE-POULENC RORER SA.  
XX  
PI Debussche L, Bracco L;  
XX  
DR WPI, 1998-272143/24.  
XX  
DR N-PSDB, V36237.  
XX  
PT Restoring p53-dependent trans-activating activity to cell containing  
mutant p53 - by delivering single-chain antibody specific for the



PA (ZENE ) ZENECA LTD.  
XX  
PI Blakey DC, Emery SC;  
XX  
DR WPI; 1999-059700/05.  
DR N-PSDB; V72059.  
XX  
PT New gene construct expressing conjugate of targeting agent and  
XX producing-converting enzyme - useful for, e.g. targeted production of  
XX cytotoxic drug in vivo, especially for treatment of cancer  
XX  
PS Example 14; Page 78-79; 100pp; English.  
XX  
CC This sequence is used in a method for obtaining a novel gene construct  
CC (A) which expresses, in cells of a mammal, a conjugate (B) of a  
CC cell-targeting group (I) and a heterologous prodrug-converting enzyme  
CC (II), and (B) is directed to leave the cell for selective localisation at  
CC a cell surface antigen (Ag) recognised by (I). Delivery of (A) to a  
CC target site, then administration of (II) is used for targeted release of  
CC cytotoxic drug, specifically for treating cancer but also inflammation  
CC such as rheumatoid arthritis. In situ generation of the targeting  
CC antibody increases selectivity, reducing side effects at normal tissue.  
CC The method is applicable to any antibody-directed enzyme prodrug therapy  
CC system.  
CC  
XX Sequence 673 AA;  
SQ  
Query Match 77.9%; Score 1024.5; DB 20; Length 673;  
Best Local Similarity 77.9%; Pred. No. 8.5e-67;  
Matches 194; Conservative 21; Mismatches 33; Indels 1; Gaps 1;  
QY 1 OVKQESGAEIVRSGASVNLSCASGFNIDYIMHWKORPEGLEWIGYIDPESGETEY 60  
DB 20 qvqlqggaellvxpqasvlgscaksgyftgylhvwkqrpqgglewlgvmpstgrsdy 79  
QY 61 APNFGKATVTADTSSNTALHLSLSEDTYYCNAVIYEXDYGALDYWGOGTIVY 120  
DB 80 nefkfnkatltvksstetajmqsltsedavaycarerayydd-andywgqgtltv 138  
QY 121 SSGGGGSGGGGSGGSDIELTQSPSSLAVSAGEKVMASCKSSQSLFNSTRKNYLAWYQ 180  
DB 139 ssgsgsgsgsgsgsgsgsdieqlsgpslavsaqekvmcskssqslfnstrknylawyq 198  
QY 181 QKRGQSPKVIIVASTRESGVDPDRFTSGSGDTFTLTSSVOAEDLAIVYCKOSYNLPTF 240  
DB 199 qrpqgspkrllyvawstltsvgpdrftgsgsgdtftltssvgaedlaivycqsytlrft 258  
QY 241 GGCTKLEIK 249  
DB 259 ggggtkleik 267  
RESULT 4  
ID W60769 standard; Protein: 243 AA.  
XX W60769;  
XX  
XX 08-SEP-1998 (first entry)  
XX  
DE Single chain antibody (ScFv) 421 that binds to mutant p53 proteins.  
XX  
XX  
XX Single chain antibody; ScFv 421; mouse; p53 protein; oligomerisation;  
XX regulatory domain; p53 mutant; H273; W248; G281;  
XX p53-dependent trans-activating activity; restoration;  
XX tumour-suppressing activity; tumour cell; treatment;  
XX hyper-proliferation; cancer; re-stenosis; ss.  
XX  
XX Mus sp.  
XX  
XX WO9818825-A1.  
XX

PD 07-MAY-1998.  
XX  
XX 27-OCT-1997; 97WO-FR01921.  
XX  
XX 29-OCT-1996; 96FR-0013176.  
XX  
XX (RHON ) RHONE-POULENC RORER SA.  
XX  
XX Debussche L, Bracco L;  
XX  
XX WPI; 1998-272140/24.  
XX  
XX N-PSDB; V36236.  
XX  
PT Restoring p53-dependent trans-activating activity to cell containing  
XX mutant p53 - by delivering single-chain antibody specific for the  
XX mutant, particularly for treatment of tumours  
XX  
XX Claim 5; Page 31; 54pp; French.  
XX  
CC The present sequence represents a single chain antibody (ScFv) designated  
CC 421. The antibody binds to an epitope present in the C-terminal region  
CC of the p53 protein that includes oligomerisation and regulatory domains,  
CC specifically between positions 320 and 393. ScFv 421 is directed against  
CC p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is  
CC introduced into cells containing a mutant p53 protein, p53-dependent  
CC trans-activating activity is restored. ScFv 421 is specific for  
CC p53-mutants that have lost tumour-suppressing activity and are present in  
CC tumour cells. It is particularly used to treat hyper-proliferation  
CC associated with these mutants (e.g. cancer and re-stenosis) but may also  
CC be used in vitro for studying mechanisms of activity of p53 or its mutant  
CC and to purify or detect p53.  
XX  
SQ Sequence 243 AA;  
Query Match 73.1%; Score 961; DB 19; Length 243;  
Best Local Similarity 74.8%; Pred. No. 1.1e-62;  
Matches 187; Conservative 23; Mismatches 32; Indels 8; Gaps 3;  
QY 1 OVKQESGAEIVRSGASVNLSCASGFNIDYIMHWKORPEGLEWIGYIDPESGETEY 60  
DB 1 qvqlqggaellvxpqasvlgscaksgyftgylhvwkqrpqgglewlgvmpstgrsdy 79  
QY 61 APNFGKATVTADTSSNTALHLSLSEDTYYCNAVIYEXDYGALDYWGOGTIVY 120  
DB 61 aprtqgkatmtadtsntalytqsltsedavaycarerayydd-andywgqgtltv 138  
QY 121 SSGGGGSGGGGSGGSDIELTQSPSSLAVSAGEKVMASCKSSQSLFNSTRKNYLAWYQ 180  
DB 115 ssgsgsgsgsgsgsgsgsdieqlsgpslavsaqekvmcskssqslfnstrknylawyq 198  
QY 181 QKRGQSPKVIIVASTRESGVDPDRFTSGSGDTFTLTSSVOAEDLAIVYCKOSYNLPTF 240  
DB 174 qrpqgspkrllyvawstltsvgpdrftgsgsgdtftltssvgaedlaivycqsytlrft 258  
QY 240 FGCTKLEIK 249  
DB 234 fgggtkleik 243  
RESULT 5  
ID W28491 standard; Protein: 535 AA.  
XX W28491;  
XX  
XX 25-NOV-1997 (first entry)  
XX  
DE Human p53 protein variant S-325 encoded by pBC176.  
XX  
XX  
XX Leucine zipper domain; LZD; oligomerisation domain; mutant; mutin;  
XX substitution; replacement; transactivation; viral protein VP16; HSV;  
XX anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;  
XX

KM tumour suppression; apoptosis; single chain antibody variable domain.  
 XX Chimeric - Homo sapiens.  
 OS Chimeric - Herpes simplex virus.  
 OS Synthetic.

PN WO9704092-A1.

PD 06-FEB-1997.

PF 17-JUL-1996; 96WO-FR01111.

PR 19-JUL-1995; 95FR-0008729.

PA (RHON ) RHONE-POULENC RORER SA.

PI Bracco L, Conseiller E;

DR WPI; 1997-132633/12.

DR N-PSDB; T86221.

PT New p53 variants e.g. with oligomerisation domain replaced by  
 PT leucine zipper - useful for treating hyper-proliferative disorders,  
 PT esp. cancer and restenosis

PS Claim 36; Pages 88-90; 133pp; French.

XX Claimed variants of protein p53 have at least part of the  
 CC oligomerisation domain deleted and replaced by a leucine zipper  
 CC domain. The mutants preferably also have at least part of the p53  
 CC transactivation domain (amino acids 1-74) deleted and replaced by  
 CC the transactivating domain (TD) from herpes simplex virus viral  
 CC protein VP16 (amino acids 411-490) or by a protein domain able to  
 CC bind selectively to a transactivator, especially a single-chain  
 CC antibody variable domain (ScFv). The present sequence is that of  
 CC a specifically claimed p53 variant designated S-325 and comprising  
 CC a ScFv domain, amino acids 75-325 of human wild-type p53 and a  
 CC leucine zipper domain at the C-terminal. The p53 variants are  
 CC more active and more stable tumour suppressors and apoptosis-inducing  
 CC agents than wild-type p53 and are active where the wild-type protein  
 CC is not, i.e. they are not inactivated by dominant negative or oncogenic  
 CC mutants, nor by other cellular proteins (because the leucine zipper  
 CC domain prevents formation of inactive mixed oligomers).

XX Sequence 535 AA;

Query Match 72.6%; Score 955; DB 18; Length 535;

Best Local Similarity 74.4%; Pred. No. 7.2e-62; Indels 8; Gaps 3;  
 Matches 186; Conservative 23; Mismatches 33;

QY 1 QVKLOESGAELVRSASVNLSCASGFNFKDYMHVWKORPEGLEWIGYIDPESGETEY 60  
 DB 3 qvqlqesgaeivsgasvsklscasgfnkdyhmwvkqpegglewlgwldpengdtey 62  
 QY 61 APNFOGKATYATDTSNTAYLHLSLSEDTYYVCNAVITYEYDGYALDYWGQGTIVTV 120  
 DB 63 apfifqgkatmtadtsntaylqlslasedtavycc-----fygdaldywgqgtitv 116  
 QY 121 SSGGGGGGGGGGGSDIELTOSPSLAYSAGEKVMSCSSSLNSKTRKNTLAWYQ 180  
 DB 117 ssgggggggggggssdieltospslayasagekvmsckssslnsktrkntlawnll 175  
 QY 181 QKPGOSKPVITYASTRESGVDPDRFTSGSGSDPTFTLTISSVOAEDLAVYCKOSYNLP-T 229  
 DB 176 qrpqgsqskrlilylvskldsyvprftfsgsgsdptftlklnrveadlgvyvycwqgtthp 235  
 QY 240 FGGGTKLKIR 249  
 DB 236 fgggtklkirk 245

RESULT 6

W28492  
 ID W28492 standard; Protein; 535 AA.

XX W28492;

XX 25-NOV-1997 (first entry)

XX Human p53 protein variant S-325H.

XX Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;  
 KW substitution; replacement; transactivation; viral protein VP16; HSV;  
 KW anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;  
 KW tumour suppression; apoptosis; single chain antibody variable domain.

XX Chimeric - Homo sapiens.

XX Chimeric - Herpes simplex virus.

XX Synthetic.

XX Key Location/Qualifiers

XX MISC-difference 361

XX /note= "Arg residue at position 182 of wild-type

XX p53 has been mutated to His"

XX WO9704092-A1.

XX 06-FEB-1997.

XX 17-JUL-1996; 96WO-FR01111.

XX 19-JUL-1995; 95FR-0008729.

XX (RHON ) RHONE-POULENC RORER SA.

XX Bracco L, Conseiller E;

XX WPI; 1997-132633/12.

XX New p53 variants e.g. with oligomerisation domain replaced by

XX leucine zipper - useful for treating hyper-proliferative disorders,

XX esp. cancer and restenosis

XX Claim 36; Page -; 133pp; French.

XX Claimed variants of protein p53 have at least part of the  
 CC oligomerisation domain deleted and replaced by a leucine zipper  
 CC domain. The mutants preferably also have at least part of the p53  
 CC transactivation domain (amino acids 1-74) deleted and replaced by  
 CC the transactivating domain (TD) from herpes simplex virus viral  
 CC protein VP16 (amino acids 411-490) or by a protein domain able to  
 CC bind selectively to a transactivator, especially a single-chain  
 CC antibody variable domain (ScFv). The present sequence is that of  
 CC a specifically claimed p53 variant designated S-325H and comprising  
 CC a ScFv domain, amino acids 75-325 of human wild-type p53 (but with  
 CC Arg182 replaced by His) and a leucine zipper domain at the C-terminal.  
 CC The p53 variants are more active and more stable tumour suppressors  
 CC and apoptosis-inducing agents than wild-type p53 and are active where  
 CC the wild-type protein is not, i.e. they are not inactivated by dominant  
 CC negative or oncogenic mutants, nor by other cellular proteins (because  
 CC the leucine zipper domain prevents formation of inactive mixed  
 CC oligomers).

CC (Note: this sequence does not appear in the specification and has  
 CC been produced by modifying the given sequence of variant V-325).

XX Sequence 535 AA;

Query Match 72.6%; Score 955; DB 18; Length 535;

Best Local Similarity 74.4%; Pred. No. 7.2e-62; Indels 8; Gaps 3;  
 Matches 186; Conservative 23; Mismatches 33;

QY 1 QVKLOESGAELVRSASVNLSCASGFNFKDYMHVWKORPEGLEWIGYIDPESGETEY 60  
 DB 3 qvqlqesgaeivsgasvsklscasgfnkdyhmwvkqpegglewlgwldpengdtey 62

```

OY 61 APNFGKATVADTSSNTAYLHLSLTSEDITVYVCNAVITYEYDGYALDYGOGTTVY 120
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 apkfgkatmtcdtsntylqlssasedtavyccn-----fygdaldygggtttvv 116
OY 121 SSGGGSGGGGGGGSDIELTQSPSSLAVSAGEVAMSCSKSSQSLFNSRTRKNYLAWQ 180
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 117 ssqggsgsgsgsgsdvltmctptltsltlgqpsasickssqsllds-dgktylnwll 175
OY 181 QKPGGSPKVLITWASTREGVDPDRFTGSGSGDTFTLTSSVQAEADLAAYYCKQSYNLP-T 239
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 176 qrpqgspklllyvskldsgvdpdrftgsgsgdftlknrvaeedlgyycwqgthspilt 235
OY 240 FCGGTRLEIK 249
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 236 fgaqtkleik 245

RESULT 7
W90217
ID W90217 standard; Protein; 580 AA.
XX W90217;
XX 10-MAY-1999 (first entry)
DE Bispecific tetraivalent antibody B1TAB7-24-IG10H6.
XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
XX CD86; T cell activation; inhibitor; graft versus host disease;
XX transplant rejection; allograft rejection; autoimmune disease;
XX allergy; therapy: human; bispecific tetraivalent antibody; B1TAB;
XX B1TAB7-24-IG10H6.
XX Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
OS Chimeric - synthetic.
XX Key Location/Qualifiers
FH Peptide 1..24
    /note= "peab signal peptide"
FH Region 25..138
    /note= "VH region anti B7.1 Mab"
FH Peptide 139..153
    /note= "(GAS3) flexible linker"
FH Region 154..262
    /note= "VL region anti B7.1 Mab"
FH Region 263..273
    /note= "human IgG3 hinge region"
FH Domain 274..308
    /note= "helix-turn-helix dimerisation domain"
FH Domain 309..319
    /note= "human IgG3 hinge domain"
FH Region 320..446
    /note= "VH region anti B7.2 Mab"
FH Peptide 447..461
    /note= "(GAS3) flexible linker"
FH Region 462..574
    /note= "VL region anti B7.2 Mab"
FH Peptide 575..580
    /note= "His6 tag"
FH Misc-difference 261
    /note= "encoded by CPG"
FH Misc-difference 322..327
    /note= "codons for these amino acids are not
    present in the DNA sequence for
    B1TAB7-24-IG1-H6 provided in the
    specification"
XX W09858965-A2.
XX 30-DEC-1998.
XX

```

```

PF 22-JUN-1998; 98WO-EP03791.
XX
XX 20-JUN-1997; 97EP-0870092.
XX
XX (INNO-) INNOGENETICS NV.
PA
XX Bosman A, Buysse M, Loree K, Sablon E;
PI WPI: 1999-105615/09.
XX N-PSDB; X01651.
DR
XX
XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
PI immune diseases including allograft rejection
PT
XX
XX Example 7.1; Fig 16; 182pp; English.
PS
XX
XX This polypeptide comprises the bispecific tetraivalent antibody
CC B1TAB7-24-IG10H6. The molecule consists of 4 scfvs, i.e. 2
CC anti B7.1 scfvs and 2 anti B7.2 scfvs (tetravalency). One single
CC B1TAB is a homodimer of 2 identical molecules, each containing both
CC an anti B7.1 and anti B7.2 scfv (bispecificity). An anti-B7.1 and
CC and anti-B7.2 scfv are linked using a dimerisation domain (see
CC W90219), which drives the homodimerisation of the molecule. DNA
CC (see X01651) encoding the B1TAB has been constructed to allow
CC expression of the B1TAB in transformed E. coli cells. The B1TAB
CC cross-links, and/or cross-reacts, with the costimulatory molecules
CC B7.1 and B7.2 that are expressed on the membrane of professional
CC antigen-presenting cells, leading to the inhibition of antigen-
CC specific T cell activation. The invention relates to such
CC B7-binding molecules, methods for their production, and their use
CC for treating or preventing diseases of the immune system, in
CC particular graft rejection, graft versus host disease, allergy and
CC autoimmune diseases (claimed).
XX
XX Sequence 580 AA:
SQ

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Query Match 72.3%; Score 951; DB 20; Length 580;
Best Local Similarity 73.5%; Pred. No 1.5e-61;
Matches 183; Conservative 22; Mismatches 44; Indels 0; Gaps 0;

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```

OY 1 QVKLOESGAELVRSAGSYNLSTASGFNIKDYMMWVQRPESGLEWITGIDPESGETEY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 325 qvqlqsgspellekpgasvkiskcasgyftgmmwvqngskslwlgldpyrgstys 384
OY 61 APNFGKATVADTSSNTAYLHLSLTSEDITVYVCNAVITYEYDGYALDYGOGTTVY 120
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 385 npklegkatlvtvdkssstlaymqlstedsavycarfaygydylymdywgsgttvtv 444
OY 121 SSGGGSGGGGGSDIELTQSPSSLAVSAGEVAMSCSKSSQSLFNSRTRKNYLAWQ 180
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 445 ssqggsgsgsgsgsdvltmctptltsltlgqpsasickssqsllds-dgktylnwll 504
OY 181 QKPGGSPKVLITWASTREGVDPDRFTGSGSGDTFTLTSSVQAEADLAAYYCKQSYNLP-T 240
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 505 qrpqgspklllyvskldsgvdpdrftgsgsgdftlknrvaeedlgyycwqgthspilt 564
OY 241 GCGTRLEIK 249
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 565 ggaqtkleik 573

RESULT 8
W90218
ID W90218 standard; Protein; 556 AA.
XX W90218;
XX 10-MAY-1999 (first entry)
DE Bispecific tetraivalent antibody B1TAB1G10-B7-24H6.
XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
XX

```

KW CD86; T cell activation; inhibitor; graft versus host disease;  
 KW transplant rejection; allograft rejection; autoimmune disease;  
 KW allergy; therapy; human; bispecific tetraivalent antibody; B17Ab;  
 KW B17Ab1G10-B7-24H6.  
 XX  
 OS Chimeric - Mus sp.  
 OS Chimeric - Homo sapiens.  
 OS Chimeric - synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..120 "VH region anti B7.2 MAb"  
 FT Peptide /note="VH region anti B7.2 MAB"  
 FT 121..135  
 FT /note="(G4S3) flexible linker"  
 FT 136..248  
 FT /note="VL region anti B7.2 MAB"  
 FT 249..259  
 FT /note="human IgG3 hinge region"  
 FT 260..285  
 FT /note="helix-turn-helix dimerisation domain"  
 FT 286..305  
 FT /note="human IgG3 hinge domain"  
 FT 306..426  
 FT /note="VH region anti B7.1 MAB"  
 FT 427..441  
 FT /note="(G4S3)flexible linker"  
 FT 442..550  
 FT /note="VL region anti B7.1 MAB"  
 FT 551..556  
 FT /note="His6 tag"  
 FT Peptide  
 PN W09858965-A2.  
 XX  
 PD 30-DEC-1998.  
 XX  
 PE 22-JUN-1998; 98WO-EP03791.  
 XX  
 PR 20-JUN-1997; 97EP-0870092.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Bosman A, Buyse M, Lorre K, Sablon E;  
 DR WPI: 1999-105615/09.  
 DR N-PSDB; X01652.  
 XX  
 PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat  
 PT immune diseases including allograft rejection  
 XX  
 PS Example 7.1: Fig 18; 182pp; English.  
 XX  
 CC This polypeptide comprises the bispecific tetraivalent antibody  
 CC B17Ab1G10-B7-24H6. The molecule consists of 4 scFvs, i.e. 2  
 CC anti B7.1 scFvs and 2 anti B7.2 scFvs (tetravalency). One single  
 CC B17Ab is a homodimer of 2 identical molecules, each containing both  
 CC an anti B7.1 and anti B7.2 scFv (bispecificity). An anti-B7.1 and  
 CC and anti-B7.2 scFv are linked using a dimerisation domain (see  
 CC W90219), which drives the homodimerisation of the molecule. DNA  
 CC (see X01652) encoding the B17Ab has been constructed to allow  
 CC expression of the B17Ab in transformed E. coli cells. The B17Ab  
 CC cross-links, and/or cross-reacts, with the costimulatory molecules  
 CC B7.1 and B7.2 that are expressed on the membrane of professional  
 CC antigen-presenting cells, leading to the inhibition of antigen-  
 CC specific T cell activation. The invention relates to such  
 CC B7-binding molecules, methods for their production, and their use  
 CC for treating or preventing diseases of the immune system, in  
 CC particular graft rejection, graft versus host disease, allergy and  
 CC autoimmune diseases (claimed).  
 CC  
 SQ Sequence 556 AA:

Query Match; 71.6%; Score 942; DB 20; Length 556;

Best Local Similarity 73.3%, Pred. No. 6.5e-61;  
 Matches 181; Conservative 22; Mismatches 44; Indels 0; Gaps 0;  
 QY 3 KLOESGAEIIVHSGASVNSCTASGSEINIKDYVMHWKORPEEGLEWIGYDPESGETEYAP 62  
 Db 1 q1qgsapelekpgasvskscasgysftgmmwvwxgngsklewtgldpyggstsynp 60  
 QY 63 NFOKATVTAJPTSSNTAVLHLSLSEDTTYYCNNAVITYEYDGYALDYWGOGTTVTYSS 122  
 Db 61 kiegkeltlvdkssstajymqlesltsedsavyycaarfaygdgyyldmywgstctvss 120  
 QY 123 GCGGSGGSGGSGGSDIELTQSPSSLAWSAGEKVMASCSQSLNSRKRYTLAYQOK 182  
 Db 121 gggsgsgsgsgsdieitqspsslawageevmtckssqsvlyssnqknylawyqgk 180  
 QY 183 PGSPKVLITYMASTPESGVDPDRFTGSGGSDTFLTITSSVQAADLVVYCKOSYNLPTFGG 242  
 Db 181 pgspkillyvastresgvdpdrftgsgsdltstssqaedlavyychnqylswtfg 240  
 QY 243 GYKLEIK 249  
 Db 241 gtlkleik 247  
 RESULT 9  
 W37738  
 ID W37738 standard; Protein: 437 AA.  
 XX  
 AC W37738;  
 XX  
 DT 07-JUL-1998 (first entry)  
 XX  
 DE Nucleotide sequence encoding the Mgr6-clavin immunotoxin.  
 KW Recombinant ribosomal inhibitor protein; RIP; clavin; inhibition;  
 KW protein synthesis; conjugate; Mgr6-clavin; anticancer; antiviral agent.  
 XX  
 OS Chimeric - Aspergillus clavatus.  
 OS Chimeric - Mus musculus  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 96..286  
 FT /note="Mgr6 from M. musculus"  
 FT 287..437  
 FT Peptide /note="Clavin from A. clavatus"  
 XX  
 PN W09749726-A1.  
 XX  
 PD 31-DEC-1997.  
 XX  
 PF 26-JUN-1997; 97WO-EP03359.  
 XX  
 PR 27-JUN-1996; 96IT-FI00155.  
 XX  
 PA (ITUV-) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.  
 XX  
 PI Colnaghi M, De Santis R, Mele A, Parente D;  
 DR WPI: 1998-077109/07.  
 DR N-PSDB; V09256.  
 XX  
 PT DNA encoding Aspergillus clavatus-derived ribosomal inhibitor  
 PT protein, clavin - useful as an immuno-conjugate and for treatment of  
 PT cancer  
 XX  
 PS Claim 4: Pages 14-15; 26pp; English.  
 XX  
 CC This is the amino acid sequence of a fusion protein consisting of the  
 CC Mgr6 single chain antibody (with the heavy and light chain joined by  
 CC a linker), fused to the clavin protein. Clavin is an inhibitor  
 CC protein, and functions by inactivating the ribosomes. Clavin or its  
 CC conjugates are useful as anticancer and/or antiviral agents. The  
 CC recombinant ribosomal inhibitor protein (RIP), Mgr6-clavin (a conjugate



PS Claim 27; Fig 6.10; 152pp; English.

XX The invention relates to a method of identifying binding site domains  
 CC (BSD) that retain the capacity of binding to a predetermined epitope when  
 CC positioned C-terminal of at least one further domain in a recombinant bi-  
 CC or multivalent polypeptide. The method comprises (a) testing a panel of  
 CC BSD displayed on the surface of a biological display system as part of a  
 CC fusion protein for binding to a predetermined epitope, where the fusion  
 CC protein comprises an additional domain positioned N-terminal of the BSD  
 CC and an amino acid sequence that mediates anchoring of the fusion protein  
 CC to the surface of the display system; and (b) identifying a BSD that  
 CC binds to the predetermined epitope. The method is useful to identify bi-  
 CC or multivalent polypeptides that comprise antibody binding sites capable  
 CC of efficiently binding to the corresponding antigen. The polypeptides or  
 CC antibodies identified by the method are useful therapeutically and  
 CC diagnostically, for e.g. cancer and autoimmune diseases. scFv-antibody  
 CC fragments that bind independently of their position within bifunctional  
 CC single-chain fusion proteins can be isolated from combinatorial antibody  
 CC libraries using the new in vitro method. Sequences Y1/957-965 represent  
 CC mouse scFv fragments.

SO Sequence 248 AA:

Query Match 70.0%; Score 921; DB 20; Length 248;  
 Best Local Similarity 71.7%; Pred. No. 9e-60;  
 Matches 177; Conservative 25; Mismatches 41; Indels 4; Gaps 2;

QY 4 LOSSGAEIVKSGASVNLSCASGFNFKDYMHVWKORPEGLMIGYIDPESGETEAPN 63  
 Db 5 leqsgaelvypgtsvxlscasgafnfywlgvkkp9hglewlgdlfp9sgnlhynek 64  
 QY 64 FQKATVADTSSNTAVLHLSLTSEDTTYVCNAVYYEYDGYALDYMGGTTVYSSG 123  
 Db 65 fkgkaltldksstymqslstfedsayfcarlnw---epndywgqgtvtvssg 121  
 QY 124 GGGSGGGSGGSDIELTOSPSLAVSAGEKYAMCKSSQSLFNSRTKKNYLAWQKP 183  
 Db 122 gggsgggsggsgelvtmgtspslvtagekytmsckssqslinsgnkyltwyqgkx 181  
 QY 184 GQPKVLIWASTRESGVPRFTGSGSGTDFTLTSSVOAEDLAVYCKOSYMLP-TFGG 242  
 Db 182 gqpkvlllwastresgvprftgsgsgtdftltssvgaedlavyycqndysyplftga 241  
 QY 243 GTRKLEIK 249  
 Db 242 gtrkleik 248

RESULT 12  
 W82744  
 ID W82744 standard; Protein: 281 AA.  
 XX  
 AC W82744;  
 XX  
 DT 10-MAY-1999 (first entry)  
 XX  
 DE Fusion protein pIC1266/8061scfvtg/his.  
 XX  
 KW Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;  
 KW produg-converting enzyme; cell surface antigen; treatment; cancer;  
 KW inflammation; rheumatoid arthritis; antibody; produg therapy system.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9851787-A2.  
 XX  
 PD 19-NOV-1998.  
 XX  
 PF 05-MAY-1998; 98WO-GB01294.  
 XX  
 PR 10-MAY-1997; 97GB-0009421.  
 XX

PA (ZENEC) ZENECA LTD.  
 XX  
 PI Blakey DC, Emery SC;  
 XX  
 DR WPI: 1999-059700/05.  
 XX  
 DR N-PSDB; V72069..

PT New gene construct expressing conjugate of targeting agent and  
 PT produg-converting enzyme - useful for, e.g. targeted production of  
 PT cytotoxic drug in vivo, especially for treatment of cancer.

XX Example 16; Page 84-85; 100pp; English.

XX This sequence is a used in a method for obtaining a novel gene construct  
 CC (A) which expresses, in cells of a mammal, a conjugate (B) of a  
 CC cell-targeting group (I) and a heterologous produg-converting enzyme  
 CC (II), and (B) is directed to leave the cell for selective localisation  
 CC at a cell surface antigen (Ag) recognised by (I). Delivery of (B) to a  
 CC target site, then administration of (II) is used for targeted release of  
 CC cytotoxic drug, specifically for treating cancer but also inflammation  
 CC such as rheumatoid arthritis. In situ generation of the targeting  
 CC antibody increases selectivity, reducing side effects at normal tissue.  
 CC The method is applicable to any antibody-directed enzyme produg therapy  
 CC system.

SO Sequence 281 AA:

Query Match 68.9%; Score 906; DB 20; Length 281;  
 Best Local Similarity 69.2%; Pred. No. 1.3e-58;  
 Matches 173; Conservative 30; Mismatches 37; Indels 10; Gaps 3;

QY 1 OVALQSGAEIVKSGASVNLSCASGFNFKDYMHVWKORPEGLMIGYIDPESGETEY 60  
 Db 23 evqlqsgaelvyrsgsvxlscasgafnkdymhvkkrpgglewlmwldpengdtey 82  
 QY 61 APNFOKATVADTSSNTAVLHLSLTSEDTTYVCNAVYYEYDGYALDYMGGTTVY 120  
 Db 83 apftrgkaltldksstentaylhlsstsedlavyychvillygy--landywgqgtsvav 140  
 QY 121 SSGGGSGGGSGGSDIELTOSPSLAVSAGEKYAMCKSSQSLFNSRTKKNYLAWQ 180  
 Db 141 ssgggsgggsggsgelvtmgtspslvtagekytmsckssqslinsgnkyltwyqgkx 193  
 QY 181 QKFGQSPKVLWASTRESGVPRFTGSGSGTDFTLTSSVOAEDLAVYCKOSYMLP-T 239  
 Db 194 qkfgtspkvlwystlnlasgvpafsgsgtsysaltltsmaeadaatyccqgrsypft 253  
 QY 240 FGGGTRKLEIK 249  
 Db 254 fgggtrkleik 263

RESULT 13  
 W82745  
 ID W82745 standard; Protein: 666 AA.  
 XX  
 AC W82745;  
 XX  
 DT 10-MAY-1999 (first entry)  
 XX  
 DE Fusion protein (806.077 scFv-CPG2).  
 XX  
 KW Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;  
 KW produg-converting enzyme; cell surface antigen; treatment; cancer;  
 KW inflammation; rheumatoid arthritis; antibody; produg therapy system.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9851787-A2.  
 XX  
 PD 19-NOV-1998.  
 XX







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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2001, 15:26:21 ; Search time 76.8 seconds  
(without alignments)  
489.138 Million cell updates/sec

Title: US-09-297-181-4

Perfect score: 1315

Sequence: 1 OVKLOESGAEIVRSGASVNL.....YCKGSHNPTFGGKLEIK 249

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 924906 seqs, 150866555 residues

Total number of hits satisfying chosen parameters: 924906

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/paa/PCTUS.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/paa/US06.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/paa/US07.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/paa/US08.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/paa/US081.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/paa/US082.COMB.pep:\*  
7: /cgn2\_6/ptodata/2/paa/US083.COMB.pep:\*  
8: /cgn2\_6/ptodata/2/paa/US084.COMB.pep:\*  
9: /cgn2\_6/ptodata/2/paa/US085.COMB.pep:\*  
10: /cgn2\_6/ptodata/2/paa/US086.COMB.pep:\*  
11: /cgn2\_6/ptodata/2/paa/US087.COMB.pep:\*  
12: /cgn2\_6/ptodata/2/paa/US088.COMB.pep:\*  
13: /cgn2\_6/ptodata/2/paa/US089.COMB.pep:\*  
14: /cgn2\_6/ptodata/2/paa/US090.COMB.pep:\*  
15: /cgn2\_6/ptodata/2/paa/US091.COMB.pep:\*  
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18: /cgn2\_6/ptodata/2/paa/US095.COMB.pep:\*  
19: /cgn2\_6/ptodata/2/paa/US096.COMB.pep:\*  
20: /cgn2\_6/ptodata/2/paa/US097.COMB.pep:\*  
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24: /cgn2\_6/ptodata/2/paa/US097.COMB.pep:\*  
25: /cgn2\_6/ptodata/2/paa/US097.COMB.pep:\*  
26: /cgn2\_6/ptodata/2/paa/US097.COMB.pep:\*  
27: /cgn2\_6/ptodata/2/paa/US097.COMB.pep:\*  
28: /cgn2\_6/ptodata/2/paa/US097.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1315	100.0	249	US-09-297-181-4	Sequence 4, Appli
2	961	73.1	243	US-09-297-181-2	Sequence 2, Appli
3	955	72.6	535	US-08-983-035-38	Sequence 38, Appli
4	951	72.3	580	US-09-468-029-58	Sequence 58, Appli
5	942	71.6	556	US-09-468-029-60	Sequence 60, Appli

6	923.5	70.2	242	US-09-594-985A-5	Sequence 5, Appli
7	917.5	69.8	238	US-09-559-019-28	Sequence 28, Appli
8	913.5	69.5	240	US-09-559-019-27	Sequence 27, Appli
9	906	68.9	262	US-09-594-985A-4	Sequence 4, Appli
10	897	68.2	271	US-09-594-985A-6	Sequence 6, Appli
11	896.5	68.2	272	US-09-594-985A-7	Sequence 7, Appli
12	880	66.9	268	US-09-468-029-68	Sequence 68, Appli
13	877	66.7	553	US-09-364-088-16	Sequence 16, Appli
14	877	66.7	553	US-09-523-279-16	Sequence 16, Appli
15	877	66.7	553	US-09-188-082-16	Sequence 16, Appli
16	849.5	64.6	263	US-09-468-029-76	Sequence 76, Appli
17	846	64.3	248	US-08-996-140-23	Sequence 23, Appli
18	842.5	64.1	241	US-09-202-000-8	Sequence 8, Appli
19	830	63.1	269	US-08-646-265-109	Sequence 109, App
20	830	63.1	269	US-08-646-265A-109	Sequence 109, App
21	828	63.0	238	US-09-202-000-2	Sequence 2, Appli
22	824.5	62.7	245	US-09-523-095A-40	Sequence 40, Appli
23	824.5	62.7	271	US-09-523-095A-34	Sequence 34, Appli
24	824.5	62.7	274	US-09-523-095A-32	Sequence 32, Appli
25	824	62.7	251	PCT-US00-19843-11	Sequence 11, Appli
26	824	62.7	251	PCT-US00-19843-15	Sequence 15, Appli
27	824	62.7	264	PCT-US00-19843-8	Sequence 8, Appli
28	823.5	62.6	244	US-08-553-497-20	Sequence 20, Appli
29	822.5	62.5	271	US-09-523-095A-30	Sequence 30, Appli
30	822.5	62.5	274	US-09-523-095A-26	Sequence 26, Appli
31	822	62.5	301	US-09-364-088-14	Sequence 14, Appli
32	818	62.2	301	US-09-364-088-14	Sequence 14, Appli
33	818	62.2	301	US-09-188-082-14	Sequence 14, Appli
34	816.5	62.1	242	US-08-553-497-30	Sequence 30, Appli
35	814.5	61.9	244	US-08-553-497-32	Sequence 32, Appli
36	814	61.9	273	US-09-468-029-72	Sequence 72, Appli
37	813.5	61.9	242	US-08-553-497-26	Sequence 26, Appli
38	811.5	61.7	246	US-08-553-497-24	Sequence 24, Appli
39	808.5	61.5	244	US-08-553-497-22	Sequence 22, Appli
40	803.5	61.1	259	US-09-419-788-115	Sequence 115, App
41	803.5	61.1	483	US-07-989-846B-19	Sequence 19, Appli
42	803.5	61.1	483	US-08-392-338-19	Sequence 19, Appli
43	803.5	61.1	483	US-09-443-213-19	Sequence 19, Appli
44	800.5	60.3	242	US-08-553-497-28	Sequence 28, Appli
45	799.5	60.8	241	US-09-000-802-13	Sequence 13, Appli

#### ALIGNMENTS

RESULT 1  
US-09-297-181-4  
; Sequence 4, Application US/09297181  
; GENERAL INFORMATION:  
; APPLICANT: Bracco, Laurent  
; APPLICANT: Debussche, Laurent  
; TITLE OF INVENTION: ANTI-P53 SINGLE-CHAIN ANTIBODY FRAGMENTS AND THEIR USES  
; FILE REFERENCE: ST96030-US  
; CURRENT APPLICATION NUMBER: US/09/297,181  
; CURRENT FILING DATE: 1999-04-26  
; EARLIER APPLICATION NUMBER: PCT/FR97/01921  
; EARLIER FILING DATE: 1997-10-27  
; EARLIER APPLICATION NUMBER: FR96/13176  
; NUMBER OF SEQ. ID NOS: 4  
; SOFTWARE: Patentia Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: Mgs Musculus  
US-09-297-181-4

Query Match 100.0%; Score 1315; DB 16; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1.2e+08;  
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 OVKLOESGAEIVRSGASVNLCTASGFNIKDYHMKVORPEGLWIGYIDPESGETEV 60

```
DB 1 QVKLOESGAEIVRSAGSVNLSCTASGFNIKDYMHMWKORPEEGLEWIGYIDPESGETEV 60
QY 61 APNFGKATVYADTSSNTAVYHLSTLSEDTTYVCNAVYYEYDGYALDYGOGTTVTV 120
DB 61 APNFGKATVYADTSSNTAVYHLSTLSEDTTYVCNAVYYEYDGYALDYGOGTTVTV 120
QY 121 SSGGGGGGGGGGGGSDIELTQSPSSLAWSAGEKVMASCKSSQSLFNSRTKKNYLAHQ 180
DB 121 SSGGGGGGGGGGGGSDIELTQSPSSLAWSAGEKVMASCKSSQSLFNSRTKKNYLAHQ 180
QY 181 QKPGQSPKVLIIYMASTRESGVDPDRFTGSGGTDFTLTISSVQADLAAYYCKOSYNLPTE 240
DB 181 QKPGQSPKVLIIYMASTRESGVDPDRFTGSGGTDFTLTISSVQADLAAYYCKOSYNLPTE 240
QY 241 GGGTKLEIK 249
DB 241 GGGTKLEIK 249
```

```
RESULT 2
US-09-297-181-2
; Sequence 2, Application US/09297181
; GENERAL INFORMATION:
; APPLICANT: Bracco, Laurent
; APPLICANT: Debussche, Laurent
; TITLE OF INVENTION: ANTI-P53 SINGLE-CHAIN ANTIBODY FRAGMENTS AND THEIR USES
; FILE REFERENCE: ST96030-US
; CURRENT APPLICATION NUMBER: US/09/297, 181
; CURRENT FILING DATE: 1999-04-26
; EARLIER APPLICATION NUMBER: PCT/FR97/01921
; EARLIER FILING DATE: 1997-10-27
; EARLIER APPLICATION NUMBER: FR96/13176
; EARLIER FILING DATE: 1996-10-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-297-181-2
```

```
Query Match 73.1%; Score 961; DB 16; Length 243;
Best Local Similarity 74.8%; Pred. No. 3e-77;
Matches 187; Conservative 23; Mismatches 32; Indels 8; Gaps 3;

QY 1 QVKLOESGAEIVRSAGSVNLSCTASGFNIKDYMHMWKORPEEGLEWIGYIDPESGETEV 60
DB 1 QVKLOESGAEIVRSAGSVNLSCTASGFNIKDYMHMWKORPEEGLEWIGYIDPESGETEV 60
QY 61 APNFGKATVYADTSSNTAVYHLSTLSEDTTYVCNAVYYEYDGYALDYGOGTTVTV 120
DB 61 APNFGKATVYADTSSNTAVYHLSTLSEDTTYVCNAVYYEYDGYALDYGOGTTVTV 120
QY 121 SSGGGGGGGGGGGGSDIELTQSPSSLAWSAGEKVMASCKSSQSLFNSRTKKNYLAHQ 180
DB 121 SSGGGGGGGGGGGGSDIELTQSPSSLAWSAGEKVMASCKSSQSLFNSRTKKNYLAHQ 180
QY 181 QKPGQSPKVLIIYMASTRESGVDPDRFTGSGGTDFTLTISSVQADLAAYYCKOSYNLPTE 240
DB 181 QKPGQSPKVLIIYMASTRESGVDPDRFTGSGGTDFTLTISSVQADLAAYYCKOSYNLPTE 240
QY 240 GGGTKLEIK 249
DB 240 GGGTKLEIK 249
```

```
RESULT 3
US-08-983-035-38
; Sequence 38, Application US/08983035
; GENERAL INFORMATION:
; APPLICANT: CONSEILLER, Emmanuel
```

```
APPLICANT: BRACCO, Laurent
TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSER: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegetville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983, 035
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/08729
FILING DATE: 19-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR96/01111
FILING DATE: 17-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky Esq., Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST95044-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-983-035-38
```

```
Query Match 72.6%; Score 955; DB 13; Length 535;
Best Local Similarity 74.4%; Pred. No. 2.7e-76;
Matches 186; Conservative 23; Mismatches 33; Indels 8; Gaps 3;

QY 1 QVKLOESGAEIVRSAGSVNLSCTASGFNIKDYMHMWKORPEEGLEWIGYIDPESGETEV 60
DB 3 QVKLOESGAEIVRSAGSVNLSCTASGFNIKDYMHMWKORPEEGLEWIGYIDPESGETEV 62
QY 61 APNFGKATVYADTSSNTAVYHLSTLSEDTTYVCNAVYYEYDGYALDYGOGTTVTV 120
DB 61 APNFGKATVYADTSSNTAVYHLSTLSEDTTYVCNAVYYEYDGYALDYGOGTTVTV 120
QY 121 SSGGGGGGGGGGGGSDIELTQSPSSLAWSAGEKVMASCKSSQSLFNSRTKKNYLAHQ 180
DB 121 SSGGGGGGGGGGGGSDIELTQSPSSLAWSAGEKVMASCKSSQSLFNSRTKKNYLAHQ 180
QY 181 QKPGQSPKVLIIYMASTRESGVDPDRFTGSGGTDFTLTISSVQADLAAYYCKOSYNLPTE 240
DB 181 QKPGQSPKVLIIYMASTRESGVDPDRFTGSGGTDFTLTISSVQADLAAYYCKOSYNLPTE 240
QY 240 GGGTKLEIK 249
DB 240 GGGTKLEIK 249
```

```
RESULT 4
US-09-468-029-58
; Sequence 58, Application US/09468029
; GENERAL INFORMATION:
; TITLE OF INVENTION: B7-Binding molecules for treating immune
```

	Query Match	70.2%	Score 923.5	DB 19	Length 242	
	Best Local Similarity	70.0%	Pred No 6.2e-74			
	Matches 175	Conservative 29	Mismatches 37	Indels 9	Gaps 2	
Oy	1	OVKIOESGAEIVRSGASVYLNLSCTASGAFNIDKYMHMVKORPEEGLEWIGYIDPESGETEY	60			
Dd	1	QVOLOESGAEEVKPASVAKISCKASGAYFTTDAIHMAKORPGDELMWIGYSISGNNDIR	60			
Oy	61	APNFGKATVPADTSNNRAYLTLSTLSDETTPVYYCNANVIYEYEDGALDYMGOGTTVV	120			
Dd	61	NKFNGKATLTTRDKSSSTRAYMOLNSTLSDSANVYCCKRSY-----GHMGCGTTVV	112			
Oy	121	SSGGGSGSGGSGSGGSDIELTQSPSLAVSAGEGVAMSKCSQSILFNSRTNRITLAYWQ	180			

Db 113 SSGGGGGGGGGGGSDIYVSGPSSSLPVSVGEKVTLLSCKSSQSLLYSGNKNYLAAYQ 172  
QY 181 OKPGSPKVLIIYASTRESGVDPDRFTGSGGSDIETLTITSSVQADLAAYYCKOSYNLP-T 239  
173 OKPGSPKVLIIYASTRESGVDPDRFTGSGGSDIETLTITSSVQADLAAYYCKOQYISYPLT 232  
QY 240 FGGGTRLEIK 249  
233 FGGGTRLEIK 242

## RESULT 7

US-09-559-019-28  
; Sequence 28, Application US/09559019  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; APPLICANT: Witte, Larry  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: Sequence Listings 1-34 for 381-71  
; CURRENT APPLICATION NUMBER: US/09/559,019  
; CURRENT FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO: 28  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-559-019-28

Query Match 69.8%; Score 917.5; DB 19; Length 238;  
Best Local Similarity 70.4%; Pred. No. 2.1e-73;  
Matches 176; Conservative 30; Mismatches 31; Indels 13; Gaps 4;

QY 1 OVRLQSGAEIYVSGASVNLCTASGFNIKDYMHVWKORPEGLMIGTIDPESGETEX 60  
1 OVRLQSGAEIYVSGASVNLCTASGFNIKDYMHVWKORPEGLMIGTIDPESGETEX 60  
Db 1 OVRLQSGAEIYVSGASVNLCTASGFNIKDYMHVWKORPEGLMIGTIDPESGETEX 60  
QY 61 APNFGKATVYADTSSNTAYLHLSSLTSEDPTVYVCNAVYYEYDGYALDYWGQTTVY 120  
61 APNFGKATVYADTSSNTAYLHLSSLTSEDPTVYVCNAVYYEYDGYALDYWGQTTVY 120  
Db 61 APNFGKATVYADTSSNTAYLHLSSLTSEDPTVYVCNAVYYEYDGYALDYWGQTTVY 115  
QY 121 SSGGGGGGGGGGGSDIETLTQSPSSSLAVSAGEKVMCKSSQSLFNSRTKKNYLAAYQ 180  
121 SSGGGGGGGGGGGSDIETLTQSPSSSLAVSAGEKVMCKSSQSLFNSRTKKNYLAAYQ 180  
Db 116 SSGGGGGGGGGGGSDIETLTQSPALMSASPEKVTITCSASSV-----SYMHWQ 168  
116 SSGGGGGGGGGGGSDIETLTQSPALMSASPEKVTITCSASSV-----SYMHWQ 168  
QY 181 OKPGSPKVLIIYASTRESGVDPDRFTGSGGSDIETLTITSSVQADLAAYYCKOSYNLP-T 239  
181 OKPGSPKVLIIYASTRESGVDPDRFTGSGGSDIETLTITSSVQADLAAYYCKOSYNLP-T 239  
Db 169 OKPGSPKVLIIYASTRESGVDPDRFTGSGGSDIETLTITSSVQADLAAYYCKOQYISYPLT 228  
169 OKPGSPKVLIIYASTRESGVDPDRFTGSGGSDIETLTITSSVQADLAAYYCKOQYISYPLT 228  
QY 240 FGGGTRLEIK 249  
240 FGGGTRLEIK 249  
Db 229 FGGGTRLEIK 238  
229 FGGGTRLEIK 238

## RESULT 8

US-09-559-019-27  
; Sequence 27, Application US/09559019  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; APPLICANT: Witte, Larry  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: Sequence Listings 1-34 for 381-71  
; CURRENT APPLICATION NUMBER: US/09/559,019  
; CURRENT FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO: 27  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-559-019-27

Query Match 69.5%; Score 913.5; DB 19; Length 240;  
Best Local Similarity 70.4%; Pred. No. 4.7e-73;  
Matches 176; Conservative 29; Mismatches 32; Indels 13; Gaps 4;

QY 1 OVRLQSGAEIYVSGASVNLCTASGFNIKDYMHVWKORPEGLMIGTIDPESGETEX 60  
1 OVRLQSGAEIYVSGASVNLCTASGFNIKDYMHVWKORPEGLMIGTIDPESGETEX 60  
Db 1 OVRLQSGAEIYVSGASVNLCTASGFNIKDYMHVWKORPEGLMIGTIDPESGETEX 60  
QY 61 APNFGKATVYADTSSNTAYLHLSSLTSEDPTVYVCNAVYYEYDGYALDYWGQTTVY 120  
61 APNFGKATVYADTSSNTAYLHLSSLTSEDPTVYVCNAVYYEYDGYALDYWGQTTVY 120  
Db 61 APNFGKATVYADTSSNTAYLHLSSLTSEDPTVYVCNAVYYEYDGYALDYWGQTTVY 115  
QY 121 SSGGGGGGGGGGGSDIETLTQSPSSSLAVSAGEKVMCKSSQSLFNSRTKKNYLAAYQ 180  
121 SSGGGGGGGGGGGSDIETLTQSPALMSASPEKVTITCSASSV-----SYMHWQ 168  
Db 116 SSGGGGGGGGGGGSDIETLTQSPALMSASPEKVTITCSASSV-----SYMHWQ 168  
QY 181 OKPGSPKVLIIYASTRESGVDPDRFTGSGGSDIETLTITSSVQADLAAYYCKOSYNLP-T 239  
181 OKPGSPKVLIIYASTRESGVDPDRFTGSGGSDIETLTITSSVQADLAAYYCKOSYNLP-T 239  
Db 169 OKPGSPKVLIIYASTRESGVDPDRFTGSGGSDIETLTITSSVQADLAAYYCKOQYISYPLT 228  
169 OKPGSPKVLIIYASTRESGVDPDRFTGSGGSDIETLTITSSVQADLAAYYCKOQYISYPLT 228  
QY 240 FGGGTRLEIK 249  
240 FGGGTRLEIK 249  
Db 229 FGGGTRLEIK 238  
229 FGGGTRLEIK 238

## RESULT 9

US-09-594-985A-4  
; Sequence 4, Application US/09594985A  
; GENERAL INFORMATION:  
; APPLICANT: Barbera-Guillam, Emilio  
; APPLICANT: Nelson, M. Bud  
; TITLE OF INVENTION: Vaccine formulations and methods for immunizing an  
; TITLE OF INVENTION: Individual against shed antigen-specific B cells  
; FILE REFERENCE: R-25np  
; CURRENT APPLICATION NUMBER: US/09/594,985A  
; CURRENT FILING DATE: 2000-09-12  
; PRIOR APPLICATION NUMBER: US 60/139,521  
; PRIOR FILING DATE: 1999-06-16  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: WordPerfect  
; SEQ ID NO: 4  
; LENGTH: 262  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; OTHER INFORMATION: synthesized  
US-09-594-985A-4

Query Match 68.9%; Score 906; DB 19; Length 262;  
Best Local Similarity 68.8%; Pred. No. 2.5e-72;  
Matches 172; Conservative 31; Mismatches 39; Indels 8; Gaps 2;

QY 1 OVRLQSGAEIYVSGASVNLCTASGFNIKDYMHVWKORPEGLMIGTIDPESGETEX 60  
1 OVRLQSGAEIYVSGASVNLCTASGFNIKDYMHVWKORPEGLMIGTIDPESGETEX 60  
Db 20 OVRLQSGAEIYVSGASVNLCTASGFNIKDYMHVWKORPEGLMIGTIDPESGETEX 79  
20 OVRLQSGAEIYVSGASVNLCTASGFNIKDYMHVWKORPEGLMIGTIDPESGETEX 79  
QY 61 APNFGKATVYADTSSNTAYLHLSSLTSEDPTVYVCNAVYYEYDGYALDYWGQTTVY 120  
61 APNFGKATVYADTSSNTAYLHLSSLTSEDPTVYVCNAVYYEYDGYALDYWGQTTVY 120  
Db 80 NERFKKATLTADKSSSTAYVQLNLSLSDSAVYFCTRSL-----NNAVWGQTSVTV 132  
80 NERFKKATLTADKSSSTAYVQLNLSLSDSAVYFCTRSL-----NNAVWGQTSVTV 132  
QY 121 SSGGGGGGGGGGGSDIETLTQSPSSSLAVSAGEKVMCKSSQSLFNSRTKKNYLAAYQ 180  
121 SSGGGGGGGGGGGSDIETLTQSPSSSLAVSAGEKVMCKSSQSLFNSRTKKNYLAAYQ 180  
Db 133 SSGGGGGGGGGGGSDIYVSGPSSSLPVSVGEKVTLLSCKSSQSLLYSGNKNYLAAYQ 192  
133 SSGGGGGGGGGGGSDIYVSGPSSSLPVSVGEKVTLLSCKSSQSLLYSGNKNYLAAYQ 192  
QY 181 OKPGSPKVLIIYASTRESGVDPDRFTGSGGSDIETLTITSSVQADLAAYYCKOSYNLP-T 239  
181 OKPGSPKVLIIYASTRESGVDPDRFTGSGGSDIETLTITSSVQADLAAYYCKOSYNLP-T 239  
Db 193 OKPGSPKVLIIYASTRESGVDPDRFTGSGGSDIETLTITSSVQADLAAYYCKOQYISYPLT 252  
193 OKPGSPKVLIIYASTRESGVDPDRFTGSGGSDIETLTITSSVQADLAAYYCKOQYISYPLT 252  
QY 240 FGGGTRLEIK 249  
240 FGGGTRLEIK 249



; TYPE: PRT

61 APNFGKATVTADTSSNTAYLHLSLTSEDTVYCNAYIYYEYDGAALDYMGCGTIVT 120

Db 83 NPKREGATITLVKSSSTAVMOLESLTSEDSAVYCARFAAYGDIYYIMDYGQITVTV 142  
QY 121 SSGGGGGGGGGGGGGGDIETLOSPSSLAVSAGEKVMASCKSSQSLNSRTRKNYLA 180  
Db 143 S-----SSGGGSDIELTOSPSLAVSAGEVMTCKSSOSVLYSSNQNTYLA 192  
QY 181 QKPGSPKVLITWASTRESGVDPDRFTGSGGDTFLTITSSVOAEDLAVYCKOSYNLPTF 240  
Db 193 QKPGSPKVLITWASTRESGVDPDRFTGSGGDTFLTITSSVOAEDLAVYCKOSYNLPTF 252  
QY 241 GGGTKLEIK 249  
Db 253 GGGTKLEIK 261

## RESULT 13

US-09-364-088-16  
; Sequence 16, Application US/09364088  
; GENERAL INFORMATION:  
; APPLICANT: Yashwant M. Deo, et al.  
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street, 24th floor  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/364,088  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/188,082  
; FILING DATE: 07-JUNE-1996  
; PRIOR APPLICATION DATA: US 08/484,172  
; APPLICATION NUMBER: US 08/484,172  
; FILING DATE: 07-JUNE-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Remillard, Jane E.  
; REGISTRATION NUMBER: 38,872  
; REFERENCE/DOCKET NUMBER: MXI-043CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-7414  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 553 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-364-088-16

Query Match 66.7%; Score 877; DB 17; Length 553;  
Best Local Similarity 66.5%; Pred. No. 2.4e-69;  
Matches 169; Conservative 29; Mismatches 36; Indels 20; Gaps 4;

QY 2 VKLOESGAEIVRSAGSVNLSCTASGFNIRKDYMMWVKORPEBGLWIGYIDPESGETEYA 61  
Db 278 IKLOOSGAEIVRSAGSVNLSCTASGFNIRKDYMMWVKORPEBGLWIGYIDPESGETEYA 337  
QY 62 PNFQKATVYADTSSNTAVLHLSLTSEDFTYVCNAVIYEYDG-----YALDYWGQGT 116  
Db 338 PNFQKATVYADTSSNTAVLHLSLTSEDFTYVCNAVIYEYDG-----EGIPGTGYIDYWGQGT 390

QY 117 TVTVSSGGGGGGGGGGGGGDIETLOSPSSLAVSAGEKVMASCKSSQSLNSRTRKNYL 176  
Db 391 TVTVSSGGGGGGGGGGGGGSENVLTQSPALMSASGEKVTITCSASSSV-----SYM 443  
QY 177 AMYQKPGSPKVLITWASTRESGVDPDRFTGSGGDTFLTITSSVOAEDLAVYCKOSYN 236  
Db 444 HMFQKPGSPKVLITWASTRESGVDPDRFTGSGGDTFLTITSSVOAEDLAVYCKOSYN 503  
QY 237 LP-TFEGGTLEIK 249  
Db 504 YPLTFAGTKLEIK 517

## RESULT 14

US-09-523-279-16  
; Sequence 16, Application US/09523279  
; GENERAL INFORMATION:  
; APPLICANT: Yashwant M. Deo et al.  
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED OF ANTI-FC RECEPTOR  
; TITLE OF INVENTION: BINDING AGENTS  
; FILE REFERENCE: MXI-043CP3  
; CURRENT APPLICATION NUMBER: US/09/523,279  
; CURRENT FILING DATE: 2000-03-10  
; PRIOR APPLICATION NUMBER: 09/364,088  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: 09/188,082  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: 08/661,052  
; PRIOR FILING DATE: 1996-07-07  
; PRIOR APPLICATION NUMBER: 08/484,172  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 553  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-523-279-16

Query Match 66.7%; Score 877; DB 19; Length 553;  
Best Local Similarity 66.5%; Pred. No. 2.4e-69;  
Matches 169; Conservative 29; Mismatches 36; Indels 20; Gaps 4;

QY 2 VKLOESGAEIVRSAGSVNLSCTASGFNIRKDYMMWVKORPEBGLWIGYIDPESGETEYA 61  
Db 278 IKLOOSGAEIVRSAGSVNLSCTASGFNIRKDYMMWVKORPEBGLWIGYIDPESGETEYA 337  
QY 62 PNFQKATVYADTSSNTAVLHLSLTSEDFTYVCNAVIYEYDG-----YALDYWGQGT 116  
Db 338 PNFQKATVYADTSSNTAVLHLSLTSEDFTYVCNAVIYEYDG-----EGIPGTGYIDYWGQGT 390  
QY 117 TVTVSSGGGGGGGGGGGGGDIETLOSPSSLAVSAGEKVMASCKSSQSLNSRTRKNYL 176  
Db 391 TVTVSSGGGGGGGGGGGGGSENVLTQSPALMSASGEKVTITCSASSSV-----SYM 443  
QY 177 AMYQKPGSPKVLITWASTRESGVDPDRFTGSGGDTFLTITSSVOAEDLAVYCKOSYN 236  
Db 444 HMFQKPGSPKVLITWASTRESGVDPDRFTGSGGDTFLTITSSVOAEDLAVYCKOSYN 503  
QY 237 LP-TFEGGTLEIK 249  
Db 504 YPLTFAGTKLEIK 517  
RESULT 15  
US-09-188-082-16  
; Sequence 16, Application US/09188082  
; GENERAL INFORMATION:  
; APPLICANT: Yashwant M. Deo  
; APPLICANT: Joel Goldstein  
; APPLICANT: Robert Graziano  
; APPLICANT: Cheilan Somasundaram

TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/188,082  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/661,052  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-188-082-16

Query Match 66.7%; Score 877; DB 27; Length 553;  
Best Local Similarity 66.5%; Pred. No. 2.4e-69;  
Matches 169; Conservative 29; Mismatches 36; Indels 20; Gaps 4;

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QY 62 PNEQKATVTADTSSNTATLHLSLTSEDTTYVCNAVITYEYD-----YALDIWGQGT 116  
DB 338 PFOGKATFTTIDSSNTATLQLSLTSEDTAVYYCN-----EGTPTGPFYFDYWGQGT 390  
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DEFINITION Sequence 4 from Patent WO9630512.
ACCESSION A57272 GI:3713167
VERSION A57272.1 GI:3713167
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 768)
AUTHORS Bracco, U., Schmeisnoffer, F. and Tocque, B.
TITLE CONDITIONAL EXPRESSION SYSTEM
JOURNAL Patent: WO 9630512-A 4 03-OCT-1996;
Rhone Poulenc Rorer SA (FR)
COMMENT Other publication AU 5402096 961016
Other publication FR 2732348 961004.
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 ACCESSION AJ131532  
 VERSION AJ131532.1 GI:4033863  
 KEYWORDS antibody; immunoglobulin superfamily; ScFv; variable region.  
 SOURCE Synthetic construct.  
 ORGANISM artificial construct.  
 REFERENCE 1 (bases 1 to 729)  
 AUTHORS Caron de Fromental, C., Gruel, N., Venot, C., Debussche, L.,  
 Resurrection of transcriptional activity of p53 mutants in human  
 tumour cells by intracellular expression of anti-p53 single chain  
 Fv fragments  
 JOURNAL Oncogene 18 (2), 551-557 (1999)  
 MEDLINE 99124402  
 REFERENCE 2 (bases 1 to 729)  
 AUTHORS de Fromental, C.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-DEC-1998) de Fromental C., U 380 INSERM, Institut

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VERSION	A59386.1	GI:374722	
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SOURCE		unidentified.	
ORGANISM		unclassified.	
REFERENCE		1 (bases 1 to 749)	
AUTHORS		Conseller,E. and Bracco,L.	
TITLE		P53 PROTEIN VARIANTS AND THERAPEUTICAL USES THEREOF	
JOURNAL		Patent: WO 9704092 A 36 06-FEB-1997;	
COMMENT		RHONE-POULENC RORER SA (FR)	
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Qy	541	cagaacacagagcagctctccctcaasgtctgtactctacctcggcctaccactaggaactctga	600
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VERSION	A59381.1	GI:3714713			
KEYWORDS					
SOURCE	unidentified.				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 1611)				
AUTHORS	Consellier,E. and Bracco,T.				
TITLE	P53 PROTEIN VARIANTS AND THERAPEUTICAL USES THEREOF				
JOURNAL	Patent: WO 9704092-A 31 06-FEB-1997.				
COMMENT	RHONE-POULENC ROBER SA (FR)				
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SOURCE Mus sp.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 744)
AUTHORS Kufer, P. and Raum, T.
TITLE Method of identifying binding site domains that retain the capacity
JOURNAL of binding to an epitope
Patent: WO 9925818-A 27-MAY-1999;
KUFER PETER (DE); RAUM TOBIAS (DE)
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VERSION AX003780.1 GI:99257577
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ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 744)
AUTHORS Kufer, P. and Raum, T.
TITLE Method of identifying binding site domains that retain the capacity
JOURNAL of binding to an epitope
Patent: WO 9925818-A 27-MAY-1999;
KUFER PETER (DE); RAUM TOBIAS (DE)
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QY 69 agcttcgtctcaaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaat 128
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QY 189 ctccagagcaagcactgtgactgcagacacatccctccacacagcctacactgaact 248
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JOURNAL J Immunol. Methods 178 (2), 201-209 (1995)
MEDLINE 95138549
REFERENCE 2 (bases 1 to 4354)
AUTHORS Kipriyanov,S.M., Little,M., Kropshofer,H., Breitling,F., Gotter,S.
TITLE Affinity enhancement of a recombinant antibody: formation of
complexes with multiple valency by a single-chain Fv fragment-core
streptavidin fusion
JOURNAL Protein Eng. 9 (2), 203-211 (1996)
MEDLINE 97110906
REFERENCE 3 (bases 1 to 4354)
AUTHORS Duebel,S.
TITLE Direct Submission
COMMENT Submitted (13-AUG-1997) S. Duebel, Molecular Genetics, University
of Heidelberg, Im Neuenheimer Feld 230, 69120 Heidelberg, FRG
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LOCUS AX001509 1725 bp DNA UNA 10-MAR-2000  
DEFINITION Sequence 57 from Patent WO9858965.  
ACCESSION AX001509  
VERSION AX001509.1 GI:7241662  
KEYWORDS  
SOURCE unidentified;  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 1725)  
AUTHORS Bosman, A. and Lore, K.  
TITLE B7-BINDING MOLECULES FOR TREATING IMMUNE DISEASES  
JOURNAL Patent: WO 9858965-A 30-DEC-1998;  
BOSMAN ALFONS (BE); LORE KATHRIEN (BE)  
FEATURES  
source 1..1725  
Location/Qualifiers  
BASE COUNT 424 a 439 c 468 g 394 t  
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Query Match 68.3%; Score 510.2; DB 13; Length 1725;  
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ACCESSION	A83217		
VERSION	A83217.1	GI:6732659	
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ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 2025)		
AUTHORS	Emery, S.C. and Blakey, D.C.		
TITLE	CHEMICAL COMPOUNDS		
JOURNAL	Patent: WO 9851787-A 19-NOV-1998;		
FEATURES	EMERY STEPHEN CHARLES (GB); ZENECA LTD (GB)		
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ACCESSION	AJ131195		
VERSION	AJ131195.1 GI:4138226		
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SOURCE	house mouse.		
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TITLE	Rodentia; Scurionath; Muridae; Murinae; Mus.		
JOURNAL	Bremond L., Pelissier P., Teillaud J.L., Kadenbach B., Cogne M. and		
REFERENCE	Submitted (01-DEC-1998) Bremond L., Institut de Biotechnologie,		
AUTHORS	CNRS EP118, Faculte des Sciences 123 Av. A. Thomas, 87060 Limoges Cedex, FRANCE		
TITLE	2 (bases 1 to 786)		
JOURNAL	Bremond L., Pelissier P., Teillaud J.L., Kadenbach B., Cogne M. and		
REFERENCE	nucleic acid cloning, expression and characterization of a functional		
AUTHORS	single chain immunoglobulin variable fragment (scFv) to the		
TITLE	unpublished. Encoded subunits Viac of mammalian cytochrome c oxidase		
JOURNAL	unpublished.		
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/db_xref="GI:4138227"	/db_xref="GI:4138227"		
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YEDFWGGTIVTWSGGGGGGGGGSDELTOFPSSLAVTAGEVYMRCKSSOS	YEDFWGGTIVTWSGGGGGGGGGSDELTOFPSSLAVTAGEVYMRCKSSOS		
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352..396	352..396		
misc_feature	misc_feature		
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DEFINITION	Sequence 47 from Patent WO9851787.					
ACCESSION	A83227					
VERSION	A83227.1		GI:6732667			
KEYWORDS	.					
SOURCE	unidentified.					
ORGANISM	unidentified					
	unclassified.					
REFERENCE	1 (bases 1 to 864)					
AUTHORS	Emery,S.C. and Blakey,D.C.					
TITLE	CHEMICAL COMPOUNDS					
JOURNAL	Patent: WO 9851787-A 19-NOV-1998;					
	EMERY STEPHEN CHARLES (GB); ZENECA LTD (GB)					
FEATURES	Location/Qualifiers					
source	1..864					
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Best Local Similarity	84.38;	Pred. No. 4.5e-150;		
Matches 630; Conservative	0;	Mismatches 114;	Indels 3;	Gaps 1

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Oy	61	tccttcacacgctctctgctctcaacatlaaagaactaatactgactcaggggtgaacaag	120
Db	127	tccttcacagggcttctggcctacaccttcacccggctatcgatnaccactggctgaagcagag	186
Oy	121	cctgaagagggcccttgatgtgatattgatattgatcctgagatggtgtaaacctaatat	180
Db	187	cctgacacaaaggccttgaagtggaattggaggggttaattccnagtaacggctgttgctgacac	246
Oy	181	gccccgaactccagggcacaagccacatgactgtgacagacacatcctccacaacacctac	240
Db	247	aatgacaaatttaagaaacaaagccacacactgactgtagaacaattcctccacacacgctac	306
Oy	241	ctgcacctcagcagcctgacatctgagacacaacacgctatattactgtaatgcaatcac	300
Db	307	atgcacactcagcagcctgacatctgagacacactcggcgtattactgtagaagagagag	366
Oy	301	tactatgaataagaaaggcctatgctttgtgacactctgggccaagggacacacgctaccgc	360
Db	367	gccctatggcttaccagag--atgcctatggacgactctggggccaaaggacacacgctaccgc	423
Oy	361	tcctcaggtctgagagcggttcacagcggaagtgtgctctgcgctgctgcagatcagacattg	420
Db	424	tcctcagggggcggtggcgctggggcggtgggtgggtggcggtggcggtggcggtggcggtggcg	483
Oy	421	ctcacccagctccacatcttcctgtgctgtgtcaacgagagaaagtgctctgagctgcgc	480
Db	484	ctctccacagctccacatcttcctgtgctgtgtcaacgagagaaagtgctccactgagctgc	543
Oy	481	aaatccagctcagagctgtgtcaacagtagaacccgaagaataattactgtgctgtgatacg	540
Db	544	aaatccagctcagagctgtgtcaacagtagaacccgaagaataattactgtgctgtgatacg	603
Oy	541	cagaaacacagggcagctctcctaagtgctgatactactggtgcatacactaggaatctgga	600
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Oy	601	gtccctgatgccttcaacagcagctgtgattctggaacagattcaatctcaacacagcagt	660
Db	664	gtccctgatgccttcaacagcagctgtgattctggaacagattcaatctcaacacagcagt	723

QY	661	gtcaagagctgaagccgcgcgcgttatattacgcgaagaactcttaacacagcagcttc	720
Db	724	gtcgcgcctgaagacctcgcgcatttatattacgcgaagaactcttatactcttcgacgcttc	783
QY	721	ggcgggggacccaagctcggaaatcaaa	747
Db	784	gctggaggcacaagacctcgaatgataaa	810

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LOCUS	A83211		2019 bp	DNA			
DEFINITION	Sequence 31 from Patent WO9851787.						
ACCESSION	A83211						
VERSION	A83211.1		GI:5732654				
KEYWORDS							
SOURCE	unidentified.						
ORGANISM	unidentified						
	unclassified.						
REFERENCE	1 (bases 1 to 2019)						
AUTHORS	Emery,S.C. and Blakey,D.C.						
TITLE	CHEMICAL COMPOUNDS						
JOURNAL	Patent: WO 9851787-A 19-NOV-1998;						
	EMERY STEPHEN CHARLES (GB); ZENECA LTD (GB)						
FEATURES	Location/Qualifiers						
source	1..2019						
	/organism="unidentified"						
	/db_xref="taxon:32644"						
BASE COUNT	437 a	604 c	637 g	341 t			
ORIGIN							

Query Match	73.48;	Score 548.6;	DB 81;	Length 2019;
Best Local Similarity	84.3%;	Pred. No. 4.5e-150;		
Matches 630;	Conservative	0;	Mismatches 114;	Indels 3;
				Gaps 1

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OY	61	tctctcacagcttcttgctcttaacattaaagaactacatactgcacttgcgttgcgaacagag	120
Db	118	TCTCTCAAGGCTTTGTGGCTAACTTCAACGGCTACAGTACGATACACTGGTGAAGCAGAGG	177
OY	121	cctgaagagggccctgcagcttgtagttgtatgtatattgatccctgcagagtggtggaactgaat	180
Db	178	CCTGGACAGAGCCTTTGATGGATGTGAGAGAGTTAATCCTAGTACCGGCTCTTGTCACTAC	237
OY	181	gcccgcgaacttccagggcgaaggccactgtagctgcagacacatccctccaacacagcttac	240
Db	238	AATGAGAGTGTCAAGGAACAAAGCCACACTACGTATAACAATTCCTCCACACAGCCTAC	297
OY	241	ctgcaccctcacagccctgcacatctgcagagacaacacgctctattacgttaatgcagtcac	300
Db	298	ATGCAACTCAGACACCTGACACTCTGAGAGACTTCGGGTCATTACTGTGCAAGAGAGAGG	357
OY	301	tactatgaatcacagacggtctatgctcttgcgaactgtagggccaagggaaacacgctcacgctc	360
Db	358	GCGTATGGTTGCAGC---ANGCTATGAGTACTGGGGCCAAAGGACACAGCTCACCGTC	414
OY	361	tctccaggtgtgaggcggattcaaggcggagagtggtcttcggtgcggtgcggtatcgagcatgg	420
Db	415	TCTCTCAGGTGTCGGTGGCTCGGGGGGTGGTGGGGTGGCGGGCATGTGCATTGAG	474
OY	421	ctcacccacgcttcacattctccctgcgtgtctgaagcaagaagaagtcgctatagagctgc	480
Db	475	CTCTCAGAGTCTTCATCTCTCCCTGCTGGCTGTGTGCACAGGAAGGATACCAATGAGCTGC	534
OY	481	aaatccagctcagagctcgtttaacaagtagaaccggaagaatattactggtcttgatcac	540
Db	535	AAATCCAGTCTGAGATCTCTCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGTCAG	594
OY	541	cagaacaccagggcagctctcctaagaatgctgatactactggtgcacatccaataggaatctga	600

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24 427.2 57.2 729 11 AF002242 AF002242 Mus muscu
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26 424 56.8 924 81 A62074 A62074 Sequence 9
27 424 56.8 924 81 A66044 A66044 Sequence 26
28 424 56.8 924 81 AR088013 AR088013 Sequence
29 424 56.8 930 81 A66021 A66021 Sequence 3
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31 409.6 54.8 747 11 MMYHKEG Z24480 Musculus
32 407 54.5 789 13 AX001527 AX001527 Sequence
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36 400.6 53.6 3970 12 ASY14585 Y14585 Artificial
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38 400.6 53.6 4864 12 ASY14584 Y14584 Artificial
39 400 53.5 756 81 A76868 A76868 Sequence 6
40 397.4 53.2 729 12 AX018532 AX018532 Sequence
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## ALIGNMENTS

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LOCUS Synthetic construct for anti-p53 ScFv antibody (scfvl1d3)
DEFINITION containing linker sequence.
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ACCESSION AJ131533
VERSION AJ131533.1 GI:4033867
KEYWORDS antibody; immunoglobulin superfamily; scFv; variable region.
SOURCE synthetic construct.
ORGANISM synthetic construct.
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REFERENCE 1 (bases 1 to 747)
AUTHORS Caron de Fromental,C., Gruel,N., Venot,C., Debussche,L.,
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TITLE Restoration of transcriptional activity of p53 mutants in human
tumour cells by intracellular expression of anti-p53 single chain
Fv fragments
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JOURNAL Oncogene 18 (2), 551-557 (1999)
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99124402
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2 (bases 1 to 747)
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de Fromental,C.
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Direct Submission
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```
Submitted (16-DEC-1998) de Fromental C., U 380 INSERM, Institut
```

```
Cochin de Genetique Moleculaire, 22 rue Mechain PARIS, 75014,
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FRANCE
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FEATURES
source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2,7e-208;
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BASE COUNT 189 a 188 c 205 g 165 t
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9 gccccaactcagggcagggcagcactgtgactgagacacactcctcaacagcctac 240
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11 ctcgacctcagagcctacatcctcagagacacacacgctcctactgtaatgacatc 300
12 241 CTCGACCTCAGACGCTGATCATCTAGGACACACCGCTCTATTACTGTATGACATTC 300
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14 301 TACTATGATFAGAGGCGATGCTTTGACTGTGGGCGCAAGGACACCGATACCGTC 360
15 tctctaagtgaggcgtctcaggcaggagtgctctgagcgtgtgagcagtcagatgag 420
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21 cagaacacagggcagctcctcctaagtgctgactcacttggtcactcaggaactcgtga 600
22 541 CAGAACAACGAGGCACTCTCTAAAGTGCATCTGTGGGCTCCACATAGGGAATCTGGA 600
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28 721 GCGCGGGGCGCACCAAGCTGGAATCAAA 747
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 17, 2001, 22:57:49 ; Search time 1856.43 Seconds  
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Title: US-09-297-181-3

Perfect score: 747  
Sequence: 1 caggtcaagctgcagaggtc.....gcaccaagctggaatcaaa 747

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 118133 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*  
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6: gb\_pl1:\*  
7: gb\_pl2:\*  
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12: gb\_sy:\*  
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14: em\_fun:\*  
15: em\_hum1:\*  
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19: em\_or:\*  
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85: gb\_pr8:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	747	100.0	747	12 ACO131533	AJ131533 Synthetic
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3	548.6	73.4	2019	81 A83211	A83211 Sequence 31
4	548.6	73.4	2025	81 A83217	A83217 Sequence 37
5	514.4	68.3	786	11 MMU31195	AJ131195 Mus muscu
6	510.2	68.3	1725	13 AX001509	AX001509 Sequence
7	501.6	67.1	1668	13 AX001511	AX001511 Sequence
8	471	63.1	864	12 XXU31739	U31739 Single Chat
9	469.2	62.8	4354	12 ASY14583	Y14583 Artificial
10	466	62.4	744	11 AX003772	AX003772 Sequence
11	462.8	62.0	744	11 AX003780	AX003780 Sequence
12	457.6	61.3	749	81 A59386	A59386 Sequence 36
13	457.6	61.3	1611	81 A59381	A59381 Sequence 31
14	454.4	60.3	729	12 ACO131532	AJ131532 Synthetic
15	452.8	60.5	768	81 A57272	A57272 Sequence 4
16	448.4	60.0	744	11 AX003782	AX003782 Sequence
17	447.8	59.3	723	12 AF169027	AF169027 Synthetic
18	446	59.7	1314	81 A68604	A68604 Sequence 4
19	442.4	59.2	810	81 A45006	A45006 Sequence 1
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Db     140 T T V Y V S S G G G S G G G G S G G S E N V L T O P S I M A S P E K Y T I R C S A S S Y ------S Y    192  
  
QY     176 L A W Y O Q R K G C S P X V L I Y A S T R E S G V P D R F T G S G S G D F T I T S V Q A E D A Y Y C K O S Y    235  
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Db       253 S Y P L T F G A G T K L E I K    267
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## RESULT 2

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; Sequence 70, Application US/0860174A
; Patent No. 5989830
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; GENERAL INFORMATION:
; APPLICANT: DAVIS, Paul James
; APPLICANT: VAN DER LOGT, Cornelis Paul Erik
; APPLICANT: VERHOEIJEN, Martine Elisa
; APPLICANT: WILSON, Steve
; TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
; TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
; NUMBER OF SEQUENCES: 31
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.,
; STREET: 9th Floor, East Tower
; CITY: WASHINGTON, D.C.
;
; STATE:
;
; COUNTRY: UNITED STATES
;
; ZIP: 20005-3918
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text
; SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,174A
; FILING DATE: June 16, 1997
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95307332.7
; FILING DATE: October 16, 1995
;
; APPLICATION NUMBER: PCT/EP/96/03605
; FILING DATE: August 14, 1996
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; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 282 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
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; US-08-860-174A-10

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Query Match	66.7%	Score 877.5	DB 2	Length 282
Best Local Similarity	68.0%	Pred No. 2,3e-66		
Matches 170	Conservative 20	Mismatches 57	Indels 3	Gaps 3

  

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Db	23	QVQLDESGDGLPKPGSLTL	SCATSGFTSSAFAVNRQTS	DKSLMVAITISDTITYY	.82
QY	61	APNFGKATLVADTSSNRY	LHLSLTSDTYYICNAVYY	YDGYALDDYWGQGTIVY	120
Db	83	SDNVYGRFTISDNQKNLY	LQMSLSKISDEDIVYYC	ARGGYG-KKY-PDYWGQGTIVY	140
QY	121	SSGGGSGGGGSGGGSD	IELQSPESPLVSSAGEK	AMCKSSQSLFNSRTRNYLTW	180
Db	141	SSGGGSGGGGSGGGSD	IELQSPESPLVYAGEK	YTNCKSSQSLNSVNCNYYLTW	200

QY 181 QKPCSGEVLLLYYMASTREDSGVDPDFTGSGSGTFTLLISSVQAEADLAVVYCKCKSYNLP-T 239  
Db 201 QKPGPRLTLTYMASTREDSGVDPDFRTASGSGTDETLTLISSVQAEADLAVVYCCQNDYTFPT 260  
QY 240 EGGGSKLEIK 249  
Db 261 FGGGKLEIK 270

### RESULT 3

Sequence 16, Application US/08661052  
Patent No. 5837243

GENERAL INFORMATION:

APPLICANT: Yashwant M. Deo  
APPLICANT: Joel Goldstein  
APPLICANT: Robert Graziano  
APPLICANT: Cherian Somasundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISING  
NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/661,052  
FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/484,172  
FILING DATE: 07-JUNE-1995

ATTORNEY/AGENT INFORMATION:

NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 553 amino acids  
TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-661-052-16

Query Match	66.7%	Score 877	DB 2	Length 553
Best Local Similarity	66.5%	Pred. No. 5	86-66	
Matches 169	Conservative 29	Mismatches 36	Indels 20	Gaps 4

  

QY	2	VKIQSGAELYNSSGASVNSTASGAFNTKIDYMHVAKRQPEEGLEMLGIDPESGETEYA	61
Db	278	IKIQSGAELYNSSGTSVKLSTCASAFENIKDSYMHMLRQGPQGLEMLGIDPENGDEYA	337
QY	62	PNFGKATVADPSSNTAYLHLSLSTSEDTVYVCNAVIVYEDG----	YALDWGQGT 116
Db	338	PKFGKATFTDTSNTAYLQSLSLSTSEDTAYVCN-----	EGTPTGPIYFERYEGQGT 390
QY	117	TYVYSSGGGGGGGGGGGGGSDIELTQSPSLAAGEVMAOSKSSQSLFNSTRKNYL	176
Db	391	TYVYSSGGGGGGGGGGGGGSENVLTQSPALIASAPGKATVITTSASSV-----	SYM 443
QY	177	AWYQKRGQSFVKLYIMASTRESGVDFRTGSGGCTDTLTITSSVAQADLAVYICKQSYN	236
Db	177	AWYQKRGQSFVKLYIMASTRESGVDFRTGSGGCTDTLTITSSVAQADLAVYICKQSYN	236

DB 444 HMEQKPGTSPKLMYSTNSLAVGPARFSGSGSTSYSLTISRMEADATYYCOORSS 503  
QY 237 LP-TFGGGTKLEIK 249  
DB 504 YPLTFGAGTKLEIK 517

## RESULT 4

US-08-797-689-18  
; Sequence 18, Application US/08797689  
; Patent No. 5876969  
; GENERAL INFORMATION:  
; APPLICANT: Fleer, Reinhard  
; APPLICANT: Fournier, Alain  
; APPLICANT: Guillon, Jean-Dominique  
; APPLICANT: Jung, Gerard  
; APPLICANT: Yeh, Patricia  
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,  
; TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION  
; TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, 3CA3  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: System 7.1  
; SOFTWARE: Word 5.1 (Patentin)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/797,689  
; FILING DATE: 31-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/256,927  
; FILING DATE: 28-JUL-1994  
; APPLICATION NUMBER: FR 92/01064  
; FILING DATE: 31-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR93/00085  
; FILING DATE: 28-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith Ph.D., Julie K.  
; REGISTRATION NUMBER: P-38,619  
; REFERENCE/DOCKET NUMBER: ST92006-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 454-3839  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 249 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-797-689-18

Query Match 64.1%; Score 842.5; DB 2; Length 249;  
Best Local Similarity 64.6%; Pred. No. 1.7e-63;  
Matches 164; Conservative 39; Mismatches 38; Indels 13; Gaps 4;

QY 1 QVLOESGAEVLVSGASVNLCTASGFNIKDYMHVWKORPEGLMIGYIDPESGTEY 60  
DB 4 QVLEGGSEPLVPGASVYKISCAKSGYAFGRSMNMWKORPGGLEIGRIYGGDGTXY 63  
QY 61 APMFOGKATVYADTSSNTAVLHLSLTSEDTYYC---NAVYYTYDGYALDYWGQGT 116  
DB 64 NGREFKATLADRSSSTAYMQLSLTSGSAVYFCACKENNR--FDRGYTADYWGQGT 121

QY 117 TVTVSSGGGGGGGGGGGGSDIELTQSPSLAVSAGEKVMACKSKSQSLFNSRTKRYL 176  
DB 122 TVTVSSGGGGGGGGGGGGSNQLTQSPNSMSTVGDNRVSTICKAKSQDVDS-----V 175  
QY 177 AMYQKPGQSPKLYIMASTRESGVDPRTGGSGGDTFLLTSSVQAEADLANYICKQSTN 236  
DB 176 AMYQKPGQSPKLYIMASTRYATGVDPRTGGSGGDTFLLTSSVQSEDSADYFCQOYSS 235  
QY 237 LP-TFGGGTKLEIK 249  
DB 236 YPWTFGGGTKLEIK 249

## RESULT 5

US-08-256-790-2  
; Sequence 2, Application US/08256790  
; Patent No. 5910573  
; GENERAL INFORMATION:  
; APPLICANT: PLUECKHUN, ANDREAS  
; APPLICANT: PUCK, PETER  
; TITLE OF INVENTION: MONOMERIC AND DIMERIC ANTIBODY FRAGMENT  
; TITLE OF INVENTION: FUSION PROTEINS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANTIGAN, P.C.  
; STREET: 2200 CLARENDON BLVD. SUITE 1400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,790  
; FILING DATE: 22-JUL-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP93/00082  
; FILING DATE: 15-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 92101069  
; FILING DATE: 23-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HAMLET-KING, DIANA  
; REGISTRATION NUMBER: 33,302  
; REFERENCE/DOCKET NUMBER: MERCK 1598  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-243-6333  
; TELEFAX: 703-243-6410  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 277 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-256-790-2

Query Match 63.2%; Score 831.5; DB 2; Length 277;  
Best Local Similarity 65.5%; Pred. No. 1.6e-62;  
Matches 165; Conservative 29; Mismatches 53; Indels 5; Gaps 4;

QY 1 QVLOESGAEVLVSGASVNLCTASGFNIKDYMHVWKORPEGLMIGYIDPESGE--T 58  
DB 22 EVVLVSGGGGLVPGGSLSLSCATSGFTSDPFMEVWRQPPGKRLMIAASRKAKKYYT 81  
QY 59 EYAPNFOGKATVYADTSSNTAVLHLSLTSEDTYYCNAVYYTYDGYALDYWGQGT 118  
DB 82 EYASVYKGRFVYSDTSOSITLYQNNALRAEDTAIYCC-ARNYYGSTWY-FDVGAGTIV 139



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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-553-497A-26

Query Match          61.9%: Score 813.5; DB 2: Length 242;
Best Local Similarity 64.0%: Pred. No. 4,4e-61;
Matches 160; Conservative 28; Mismatches 53; Indels 9; Gaps 3

QY 1 QVKLDESGAEALVRSASVNLCTAGFNFKKDYMMHWVKORPEEGLEWIIYIDPESEGETEY 60
DB 1 QVKLOESGAEALYKPAASVKLSCKRAGCYFTTSMHHVVKRRAOGGLEWIEINRTPATYV 60
QY 61 APNFOGKATVADITSSNTAYLHLSLTSEDITVYCNNAVITYEYDVALDYWGQGTTVV 120
DB 61 NEKFKSKATLIVDKSSSTAYMQLSSLTSEDSAYVYC-ASRDYDDGRYFDYWGQGTTVV 119
QY 121 SSGGGSGGGSGGGSGGSDIELTQSPSSSLAVSGEKVYAMSKCSQSLFNSRFRKNYLAWQ 180
DB 120 SSGGGSGGGSGGGSGGSDIELTQSPSSSLAVSGEKVYAMSKCSQSLFNSRFRKNYLAWQ 172
QY 181 QKPGSPFYLITWASTRSGVDPDRFTGSSGSDFTLTITTSVOAEDLAVYCKOSYMLP-T 239
DB 173 QKTGSPFLITDTNLSAGVYVRKSGSGISYLTITSRMRADPAATYYCQWSSYPLT 232
QY 240 FGGGTKEIK 249
DB 233 FGGGTKEIK 242

RESULT 9
US-08-553-497A-24
Sequence 24, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETTLEBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSEW, DETLEF
APPLICANT: ADAM, JAUDE
APPLICANT: MITTANS, FRANCESCA
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PIULATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: MILLEN, WHITE, ZELANO & BRANIGAN, P. C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553.497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994

```

```

: ATTORNEY/AGENT INFORMATION:
: NAME: HAMLET-KING, DIANA
: REGISTRATION NUMBER: 33,302
: REFERENCE/DOCKET NUMBER: MERCK 1726
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-243-6333
: TELEFAX: 703-243-6410
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 246 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
: US-08-553-497A-24

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Query Match	61.7%;	Score 811.5;	DB 2;	length 246;
Best Local Similarity	62.6%;	Pred. No. 6.6e-61;		
Matches 159;	Conservative 32;	Mismatches 50;	Indels 13;	Gaps 4

[illegible]

RESULT 10  
US-08-553-497A-22  
Sequence 22, Application US/08553497A  
Patent No. 5844093  
GENERAL INFORMATION:  
APPLICANT: KETTERBOROUGH, C. A.  
APPLICANT: BENDIG, MARY M.  
APPLICANT: ANSELL, KEITH H.  
APPLICANT: GUSSEW, DETLEF  
APPLICANT: ADAN, JAUME  
APPLICANT: MITJANS, FRANCESC  
APPLICANT: ROSELL, ELISABET  
APPLICANT: BLASCO, FRANCESC  
APPLICANT: PIULATS, JAUME  
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR  
TITLE OF INVENTION: ANTIBODIES  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
STREET: 2200 CLARENDON BLVD. SUITE 1400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: US  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,497A  
FILING DATE: 17-NOV-1995

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1 CLASSIFICATION: 530
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: WO PCT/EP95/00978
4 FILING DATE: 16-MAR-1995
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: EP 94104160.0
7 FILING DATE: 17-MAR-1994
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: EP 94118970.6
10 FILING DATE: 02-DEC-1994
11 ATTORNEY/AGENT INFORMATION:
12 NAME: HAMLET-KING, DIANA
13 REGISTRATION NUMBER: 33,302
14 REFERENCE/DOCKET NUMBER: MERCK 1726
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: 703-243-6333
17 TELEFAX: 703-243-6410
18 INFORMATION FOR SEQ ID NO: 22:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 244 amino acids
21 TYPE: amino acid
22 TOPOLOGY: linear
23 MOLECULE TYPE: protein
24
25 US-08-553-497A-22

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Query Match	61.5%	Score 808.5;	DB 2;	Length 244;
Best Local Similarity	62.3%	Pred. No. 1.2e-60;		
Matches 157; Conservative	32;	Mismatches 52;	Indels 11;	Gaps 3

QY	1	OVRKOECSAEIYVRSAGVNJSCFASGFINIDYVMHVKORPREGLEIGYIDESPGETEY	60
Dd	1	EVLQDSGAELIYKRGAASYKLSCRASGTFTSHMHMWKQAAGGLEIGEFNSNGRTNY	60
QY	61	APNFQGAATYADTSSNTAYLHLUSLTSEDTYYCYCAVIYIEYDGYALDYWGOGTTVY	120
Dd	61	NEKIKSATLTIVDKSSSTAYWOLSTSEDSAYYC-ASRDXDYDGDEPYWOGGTTTV	119
QY	121	SSGGSGSGGGSGGGSDIELTOSPSLAYSAEBKYAMSCSKSOSLFNSRTRKNYLAWYO	180
Dd	120	SSGGSGSGGGSGGGSGSDIELTOSPITMWSAPGEKATMTOSDBSSV-----SYAWIO	172
QY	181	OKPQSPBKVLIYMASTRESGVPDRFTGSGSGLDTFLTISSVQAEDLAYYYYCKOSYNLP--	238
Dd	173	OKTSSSRLLTYDTSNLNLSAGVPWFSSGSGGTYSXSLTISMEAEADATYYCCQOWSSYPM	232
QY	239	-TFEGGTLEIK	249
Dd	233	YTFEGGTLEIK	244

RESULT 11  
 US-08-392-338A-19  
 Sequence 19, Application US/08392338A  
 Patent No. 5863620  
 GENERAL INFORMATION:  
 APPLICANT: Whilow, Marc  
 APPLICANT: Wood, James F.  
 APPLICANT: Hardman, Karl  
 APPLICANT: Bird, Robert  
 APPLICANT: Filpula, David  
 TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Stierne, Kessler, Goldstein & Fox P.L.L.C.  
 STREET: 1100 New York Avenue, NW  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible







Sequence 19, Application US/09166094  
Patent No. 6121424  
GENERAL INFORMATION:  
APPLICANT: Whitlow, Marc  
APPLICANT: Wood, James F.  
APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert  
APPLICANT: Filpula, David  
APPLICANT: Rollence, Michelle  
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/166,094  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/392,338  
FILING DATE: 22-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.003000A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 483 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-166-094-19

Query Match 61.1%; Score 803.5; DB 3; Length 483;  
Best Local Similarity 62.4%; Pred. No. 7.1e-60;  
Matches 156; Conservative 32; Mismatches 39; Indels 23; Gaps 3;  
QY 1 OYKLOESGAEIVRSASVNLSCASGFNFKDYHMHVKNORPEGLMIGVDPESGETEY 60  
DB 128 OYOLQSDAEIVKPGASVTKISKASGITFTDRAIHVKNORPEGLMIGVDPESGNDFFK 187  
QY 61 APNFOGKATVTDTSNTAYLHLSTLSEDTVYVCNAVYYEYDGYALDYMGGCTTVV 120  
DB 188 NERFRKATLTADKSSSTAYVQLNLSLSEDSAYVFCFTRSL-----NNAVWGQTSVTV 240  
QY 121 SSGGGGGGGGGGGGSDIELTOSPPSLAVSAGEKVMASCKSSQSLFNSRTRKNYLAATQ 180  
DB 241 S-----SDVYMSQSPSLPVSVEKYTLSCSSQSILYSGNCKNYLAATQ 285  
QY 181 OKPGOSPXYLIWASTREGVPRFTGSGSGTDFTLTISVQAEADLAVYCKQSYNLP-T 239  
DB 286 QKPGOSPXYLIWASTREGVPRFTGSGSGTDFTLTISVQAEADLAVYCKQSYNLP-L 345  
QY 240 FGGGTLEIK 249

DB 346 FGGGTLEIK 355

Search completed: February 12, 2001, 15:23:46  
Job time: 60 sec

2-10 00 000

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2001, 23:01:10 ; Search time 96.92 Seconds  
(without alignments)  
2895.378 Million cell updates/sec

Title: US-09-297-181-3  
Perfect score: 747  
Sequence: 1 caggtcaagctgcagagtc.....gcaccaagctgaatcaaa 747

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 18783343 residues  
Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: /cgn2\_2/gcgdata/geneseq/NA1984.DAT:\*  
6: /cgn2\_2/gcgdata/geneseq/NA1985.DAT:\*  
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8: /cgn2\_2/gcgdata/geneseq/NA1987.DAT:\*  
9: /cgn2\_2/gcgdata/geneseq/NA1988.DAT:\*  
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12: /cgn2\_2/gcgdata/geneseq/NA1991.DAT:\*  
13: /cgn2\_2/gcgdata/geneseq/NA1992.DAT:\*  
14: /cgn2\_2/gcgdata/geneseq/NA1993.DAT:\*  
15: /cgn2\_2/gcgdata/geneseq/NA1994.DAT:\*  
16: /cgn2\_2/gcgdata/geneseq/NA1995.DAT:\*  
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18: /cgn2\_2/gcgdata/geneseq/NA1997.DAT:\*  
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21: /cgn2\_2/gcgdata/geneseq/NA2000.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	747	100.0	747	19	V36237
2	548.6	73.4	864	19	V27072
3	548.6	73.4	2019	20	V72059
4	548.6	73.4	2025	20	V72064
5	510.2	68.3	1725	20	X01651
6	504	67.5	759	19	V10378
7	501.6	67.1	1668	20	X01652
8	466	62.4	744	20	X77243
9	462.8	62.0	744	20	X77247
10	460.8	61.7	729	19	V36236
11	457.6	61.3	749	18	T86234
12	457.6	61.3	1611	18	T86221

13	452.8	60.6	768	17	T48000	Coding sequence
14	448.4	60.0	744	20	X77248	Mouse scfv fragmen
15	446	59.7	1314	19	V09256	Nucleotide sequenc
16	442.4	59.2	810	16	Q90663	MFE-23 antibody co
17	438.4	58.7	1679	18	T58130	Single chain anti-
18	438.4	58.7	1679	18	V08176	H22-anti-CEA anti-
19	435.4	58.3	804	20	X01656	Anti-B7.2 monosp
20	428.6	57.4	843	20	V72069	Fusion protein PIC
21	428.6	57.4	1998	20	V72075	Fusion protein (80
22	428	57.3	748	21	Z28962	Human anti-glycop
23	424	56.8	924	18	T94609	HindIII-EcoRI inse
24	424	56.8	924	18	T66146	scfv.4715-myc inse
25	424	56.8	930	18	T94587	EcoRI-HindIII inse
26	422.2	56.5	744	19	V11399	Human CD30 binding
27	407	54.5	789	20	X01660	Anti-B7.2 monosp
28	397.4	53.2	729	20	Z19786	Anti-5T4 secreted
29	397.4	53.2	729	20	Z07810	5T4 scfv antibody
30	397.4	53.2	1467	20	V80292	Human B7-1.5T4.1 g
31	397.4	53.2	1807	20	V80291	Anti-5T4 single ch
32	395.8	53.0	729	20	V80290	Murine anti-5T4 an
33	394.2	52.8	1518	20	V80294	B7-1/scfv specific
34	394.2	52.8	2090	20	V80295	scfv-IgE1 fusion c
35	375.4	50.3	2165	15	Q68659	CC49 VL-L-VH-L-VL-
36	375.4	50.3	2165	15	Q68660	CC49 VL-L-VH-L-VH-
37	375.4	50.3	2165	20	X25408	CC49 single chain
38	375.4	50.3	2165	20	X25409	DNA encoding a mul
39	375.4	50.3	2165	20	X15395	DNA encoding a mul
40	375.4	50.3	2165	20	X15396	DNA encoding a mul
41	373.8	50.0	726	16	T04025	Anti-BGFR single c
42	370.6	49.6	753	20	X77245	Mouse scfv fragmen
43	370.6	49.6	1637	21	Z88358	Bispecific anti-ze
44	369.4	49.5	732	16	T04020	Anti-BGFR single c
45	368.8	49.4	2478	20	X86614	cDNA encoding an a

## ALIGNMENTS

RESULT 1	V36237	standard; DNA: 747 BP.
ID	V36237	
AC	V36237	
XX		
DT	08-SEP-1998	(first entry)
DE	DNA od Scfv D3M which binds to mutant p53 proteins.	
XX		
XX	Single chain antibody; scfv D3M; mouse; p53 protein; oligomerisation;	
KW	regulatory domain; p53 mutant; H273; W248; G281;	
KW	p53-dependent trans-activating activity; restoration;	
KW	tumour-suppressing activity; tumour cell; treatment;	
KW	hyper-proliferation; cancer; re-stenosis; ss.	
OS	Mus sp.	
XX		
PN	W09818825-A1.	
PD	07-MAY-1998.	
XX		
PF	27-OCT-1997;	97WO-FR01921.
XX		
PR	29-OCT-1996;	96FR-0013176.
XX		
PA	(RHON ) RHONE-POULENC RORER SA.	
XX		
PI	Debussche L, Bracco L;	
XX		
DR	WPI: 1998-272143/24.	
XX	P-PSDB; W60770.	
PT	Restoring p53-dependent trans-activating activity to cell containing	
PT	mutant p53 - by delivering single-chain antibody specific for the	

PT mutant, particularly for treatment of tumours  
 XX  
 PS Claim 5: Page 32; 54pp; French.

CC The present sequence encodes a single chain antibody (scFv) designated  
 CC DJM. The antibody binds to an epitope present in the C-terminal region  
 CC of the p53 protein that includes oligomerisation and regulatory domains,  
 CC specifically between positions 320 and 393. scFv DJM is directed against  
 CC p53 mutants, particularly H273, W248 and G281 mutants. When the scFv is  
 CC introduced into cells containing a mutant p53 protein, p53-dependent  
 CC trans-activating activity is restored. scFv DJM is specific for  
 CC p53-mutants that have lost tumour-suppressing activity and are present in  
 CC tumour cells. It is particularly used to treat hyper-proliferation  
 CC associated with these mutants (e.g. cancer and re-stenosis) but may also  
 CC be used in vitro for studying mechanisms of activity of p53 or its mutant  
 CC and to purify or detect p53.

SQ Sequence 747 BP; 189 A; 188 C; 205 G; 165 T; 0 other;

Query Match 100.0%; Score 747; DB 19; Length 747;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-185;  
 Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caggtcaagctgacagagtcagagggcagaactgtgtgagtcaggggcctcagtcatttg 60  
 |||||  
 DB 1 caggtcaagctgacagagtcagagggcagaactgtgtgagtcaggggcctcagtcatttg 60  
 QY 61 tctctgacagctcttgcttcaacataaagatactatattgctcgtgggtgaacagagg 120  
 |||||  
 DB 61 tctctgacagctcttgcttcaacataaagatactatattgctcgtgggtgaacagagg 120  
 QY 121 ccctgaagagcgtgagtgatgtgatatattgactcctagaggtgtgtgaactgtgaat 180  
 |||||  
 DB 121 ccctgaagagcgtgagtgatgtgatatattgactcctagaggtgtgtgaactgtgaat 180  
 QY 181 gccccgaactccagaaggcacaagtcactgtgactgcagacacatcctccacaacagcc 240  
 |||||  
 DB 181 gccccgaactccagaaggcacaagtcactgtgactgcagacacatcctccacaacagcc 240  
 QY 241 ctgacactcagcagcctgacatctgagagacacaacgctctatctatctgtaagtcac 300  
 |||||  
 DB 241 ctgacactcagcagcctgacatctgagagacacaacgctctatctatctgtaagtcac 300  
 QY 301 tactatgaatacagcagcctatgcttctgactactgtgggccaagggagacacagtcac 360  
 |||||  
 DB 301 tactatgaatacagcagcctatgcttctgactactgtgggccaagggagacacagtcac 360  
 QY 361 tctctcaggtgagagcggttcagagcgagagtgctctgctggcggtggcgagatcgacatt 420  
 |||||  
 DB 361 tctctcaggtgagagcggttcagagcgagagtgctctgctggcggtggcgagatcgacatt 420  
 QY 421 ctacaccagctcctcatcttccctgctgtgtctcagcagaggaagaagtctgataagctgc 480  
 |||||  
 DB 421 ctacaccagctcctcatcttccctgctgtgtctcagcagaggaagaagtctgataagctgc 480  
 QY 481 aaatccagtcagagtcgttcaacacagtagaacccgaagaagattactgtgtgtatcag 540  
 |||||  
 DB 481 aaatccagtcagagtcgttcaacacagtagaacccgaagaagattactgtgtgtatcag 540  
 QY 541 cagaagaacagggcagctctcctaaagtgtctatctactgtggcattcagtaggaattcga 600  
 |||||  
 DB 541 cagaagaacagggcagctctcctaaagtgtctatctactgtggcattcagtaggaattcga 600  
 QY 601 gtccctgattcgtctcagagcattgtgactcgtgagacagattcactcctccacacagcagt 660  
 |||||  
 DB 601 gtccctgattcgtctcagagcattgtgactcgtgagacagattcactcctccacacagcagt 660  
 QY 661 gtccagagctgaagacctgagagcttattactgcaagaacattataatctaccagagcttc 720  
 |||||  
 DB 661 gtccagagctgaagacctgagagcttattactgcaagaacattataatctaccagagcttc 720  
 QY 721 ggcggggggcaccacagctggaatacaaa 747

DB 721 ggcggggggcaccacagctggaatacaaa 747

# RESULT 2

ID V72072 standard: DNA; 864 BP.

AC V72072;

DT 10-MAY-1999 (first entry)

DE Fusion protein pIC1266-55.1scFv tag/his DNA.

XX Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;

KW produg-converting enzyme; cell surface antigen; treatment; cancer;

KW inflammation; rheumatoid arthritis; antibody; produg therapy system; ss.

OS Synthetic.

XX WO9851787-A2.

PD 19-NOV-1998.

PF 05-MAY-1998; 98WO-GB01294.

PR 10-MAY-1997; 97GB-0009421.

PA (ZENNE) ZENBECA LTD.

PI Blakey DC, Emery SC;

DR WPI; 1999-059700/05.

PT New gene construct expressing conjugate of targeting agent and

PT produg-converting enzyme - useful for, e.g. targeted production of

PT cytotoxic drug in vivo, especially for treatment of cancer

PS Example 16; Page 86; 100pp; English.

XX This sequence is a used in a method for obtaining a novel gene construct

CC (A) which expresses, in cells of a mammal, a conjugate (B) of a

CC cell-targeting group (I) and a heterologous produg-converting enzyme

CC (II), and (B) is directed to leave the cell for selective localisation

CC at a cell surface antigen (Ag) recognised by (I). Delivery of (A) to a

CC target site, then administration of (II) is used for targeted release of

CC cytotoxic drug, specifically for treating cancer but also inflammation

CC such as rheumatoid arthritis. In situ generation of the targeting

CC antibody increases selectivity, reducing side effects at normal tissue.

CC The method is applicable to any antibody-directed enzyme produg therapy

CC system.

XX Sequence: 864 BP; 214 A; 234 C; 232 G; 184 T; 0 other;

Query Match 73.4%; Score 548.6; DB 20; Length 864;  
 Best Local Similarity 84.3%; Pred. No. 1.2e-133;  
 Matches 630; Conservative 0; Mismatches 114; Indels 3; Gaps 1;

QY 1 caggtcaagctgacagagtcagagggcagaactgtgtgagtcaggggcctcagtcatttg 60  
 |||||  
 DB 67 caggtcaagctgacagagtcagagggcagaactgtgtgagtcaggggcctcagtcatttg 126  
 QY 61 tctctgacagctcttgcttcaacataaagatactatattgctcgtgggtgaacagagg 120  
 |||||  
 DB 127 tctctgacagctcttgcttcaacataaagatactatattgctcgtgggtgaacagagg 186  
 QY 121 ccctgaagagcgtgagtgatgtgatatattgactcctgaagagtggtgaactgaatat 180  
 |||||  
 DB 187 ccctgaagagcgtgagtgatgtgatatattgactcctgaagagtggtgaactgaatat 246  
 QY 181 gccccgaactccagaaggcacaagtcactgtgactgcagacacatcctccacaacagcctac 240  
 |||||

Db	247	aatgagaagttcaagaagaanaagggccacacactgctctgtatagaacaatctctccacacacagcctac	306
Oy	241	ctgcacacctcagcagcctgacatcctcgtgaagacaacaacgctctattactcgttaatgcagctac	3000
Db	307	atgcacatccagcagcctctacacatctcgtgaagactcttcgttctattactctgcaagagagag	366
Oy	301	tactatgatcatcgcgcggtatgctcttgtagctactacgtggggccaaagggaccacaggtacacgtc	3660
Db	367	gacctatggttttcagcag--atgcatactgacatactcgtgggccaagggaccacaggtacacgtc	4223
Oy	361	tcctcaggttggaagggcgtgtctcagcgcgaaggtgctctcgtgcgttgccggtatcggacattgag	4200
Db	424	tcctcaggttgccggtgtgctcgtgcgcgt	4833
Oy	421	ctcacaccagctccatctctctccctgctgtgtgtcagcagagagagaaagtcgtctatgactgc	4800
Db	484	ctctcacagctctccatctctccctgctgtgtgtcagcagagagagaaagtcgtctatgactgc	5433
Oy	481	aaatctcagttcagagttctgtttaaacagtagaaccccgaaagaattactctggttggttacag	5400
Db	544	aaatccagctcagagttctgtttaaacagtagaaccccgaaagaattactctggttggttacag	6030
Oy	541	cagaacaacagggcagctctccccaagttgtgtatctcaccggtgcatccatccataggaattcgcga	6000
Db	604	cagaacaacagggcagctctccccaagttgtgtatctcaccggtgcatccatccataggaattcgcgg	6630
Oy	601	gtccctcgtatcgtctcacacagcagctgagatctgtgagacagattcattcattcaccatcagcag	6600
Db	664	gtccctcgtatcgtctcacacagcagctgagatctgtgagacagattcattcattcaccatcagcag	7233
Oy	661	gtcgaagcttgaagacctgagctgttatctatctgcgaacgaattctatactacacagcttc	7200
Db	724	gtcgaagcttgaagacctgagctgttatctatctgcgaacgaattctatactacacagcttc	7833
Oy	721	ggcggggggcaccacagctggaatacaaa	747
Db	784	ggtggaggcaccacagctcgaatacaaa	810
RESULT 3			
V72059			
ID	V72059	standard; DNA; 2019 BP.	
AC	V72059;		
XX	10-MAY-1999	(first entry)	
DT			
XX			
DE	Plasmid pNG4/55.1scFv/CPG2 R6 DNA.		
XX			
KW	Conjugate; cell targeting; cytotoxic drug; prodrg-converting enzyme;		
KW	cell surface antigen; treatment; cancer; inflammation; antibody;		
KW	rheumatoid arthritis; prodrg therapy system; ss.		
XX	Synthetic.		
OS			
XX			
PN	W098531787-A2.		
XX			
PD	19-NOV-1998.		
XX			
PF	05-MAY-1998; 98WO-GB01294.		
XX			
PR	10-MAY-1997; 97GB-0009421.		
XX			
PA	(ZENNE ) ZENNECA LTD.		
PI	Blakey DC, Emery SC;		
XX			
DR	WPI; 1999-059700/05.		
DR	P-PSDB; W82742.		
XX			
PT	New gene construct expressing conjugate of targeting agent and		
PT	prodrg-converting enzyme - useful for, e.g. targeted production of		
PT	cytotoxic drug in vivo, especially for treatment of cancer		

[illegible]

```
RESULT 4
ID V72064 standard; DNA: 2025 BP.
XX V72064;
AC V72064;
XX 10-MAY-1999 (first entry)
XX 10-MAY-1999 (first entry)
XX Fusion protein pNG4/55.1scfV/CPG2 R6/del EcoRI DNA.
XX Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;
XX produg-converting enzyme; cell surface antigen; treatment; cancer;
XX inflammation; rheumatoid arthritis; antibody; produg therapy system; ss.
XX Synthetic.
XX WO9851787-A2.
XX 19-NOV-1998.
XX 05-MAY-1998: 98WO-GB01294.
XX 10-MAY-1997: 97GB-0009421.
XX (ZENEC) ZENECAL LTD.
XX Blakey DC, Emery SC;
XX WPI; 1999-059700/05.
XX P-PSDB; W82743.
XX New gene construct expressing conjugate of targeting agent and
XX produg-converting enzyme - useful for, e.g. targeted production of
XX cytotoxic drug in vivo, especially for treatment of cancer
XX Example 15; Page 81; 100pp; English.
XX This sequence is a used in a method for obtaining a novel gene construct
XX (A) which expresses, in cells of a mammal, a conjugate (B) of a
XX cell-targeting group (I) and a heterologous produg-converting enzyme
XX (II), and (B) is directed to leave the cell for selective localisation
XX at a cell surface antigen (Ag) recognised by (I). Delivery of (A) to a
XX target site, then administration of (II) is used for targeted release of
XX cytotoxic drug, specifically for treating cancer but also inflammation
XX such as rheumatoid arthritis. In situ generation of the targeting
XX antibody increases selectivity, reducing side effects at normal tissue.
XX The method is applicable to any antibody-directed enzyme produg therapy
XX system.
XX Sequence 2025 BP; 440 A; 604 C; 638 G; 343 T; 0 other;
Query Match 73.4%; Score 548.6; DB 20; Length 2025;
Best Local Similarity 84.3%; Pred. No. 1.4e-133;
Matches 630; Conservative 0; Mismatches 114; Indels 3; Gaps 1;
```

```
QY 241 ctgcacctcagcagcctcgcacatctgagacacacaccgtctattactgtaatgcagtcac 300
DB 298 atgcacactcagcagcctcgcacatctgagacacacaccgtctattactgtaatgcagtcag 357
QY 301 tactatgatacgaagcgcctatcttggaactctgggcccagagacacacagtcacgcgc 360
DB 358 gccatcgtgttncagc---atgcatggaactactgggcccagagacacacagtcacgcgc 414
QY 361 tctcagcgtggagcgcgtctcagcaggtggtctgcgcgcgcgcgcgcgcgcgcgcgcgcgc 420
DB 415 tctcagcgtggagcgcgtctcagcaggtggtctgcgcgcgcgcgcgcgcgcgcgcgcgcgc 474
QY 421 ctacaccagcttcacatctccctgcgtgtgtcagcagagagagagagtcgtatgagtcgc 480
DB 475 ctctcagctctccatccctccctgcgtgtgtcagcagagagagagagtcgtatgagtcgc 534
QY 481 aatccagtcagagctgtctcacaagtagaacccgaagaatctggtcgtgtatcag 540
DB 535 aatccagtcagagctgtctcacaagtagaacccgaagaatctggtcgtgtatcag 594
QY 541 cagaacacagagcagctctcctaagtgctgactctggtcgcacacacagtaggaaatctgga 600
DB 595 cagagacacagagcagctctcctaagtgctgactctggtcgcacacacagtaggaaatctgga 654
QY 601 gtccctgacgtctcacaagcagtgatctggagacagatctcactctcaccacacagcag 660
DB 655 gtccctgacgtctcacaagcagtgatctggagacagatctcactctcaccacacagcag 714
QY 661 gtgcagcgtcgaagacacgtgcattatctcgaagcaatcttataatctaccagcgtc 720
DB 715 gtgcagcgtcgaagacacgtgcattatctcgaagcaatcttataatctaccagcgtc 774
QY 721 ggcggggggcaccagcagctggaatcaaa 747
DB 775 ggtgagggcaccagcagctggaatcaaa 801
RESULT 5
ID X01651 standard; DNA: 1725 BP.
XX X01651;
XX 10-MAY-1999 (first entry)
XX Bispecific tetraivalent antibody B1TAB724-1G10H6 DNA.
XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
XX CD86; T cell activation; inhibitor; graft versus host disease;
XX transplant rejection; allograft rejection; autoimmune disease;
XX allergy; therapy; human; bispecific tetraivalent antibody; B1TAB;
XX B1TAB7-24-1G10H6; ss.
XX Chimeric - Mus sp.
XX Chimeric - Homo sapiens.
XX Chimeric - synthetic.
XX Key Location/Qualifiers
XX CDS 1..1726
XX FT /tag- a
XX FT /transl_except= (pos:780..782, aa:11e)
XX FT /transl_except= (pos:967..969, aa:Xaa)
XX FT /note= "Xaa= Gln-Leu-Val-Gln-Val-Gln"
XX FT sig_peptide 1..72
XX FT /tag- b
XX FT /note= "pepB signal sequence"
XX FT mat_peptide 73..1726
XX FT /tag- c
XX PN MO9858965-A2.
XX 30-DEC-1998.
```









XX X77247;  
 AC 04-AUG-1999 (first entry)  
 DT Mouse scFv fragment 5-10 encoding DNA.  
 XX Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;  
 KW autoimmune disease; scFv-antibody; single-chain Fv; mouse; ss.  
 XX Mus sp.  
 OS WO925818-A1.  
 PN 27-MAY-1999.  
 PD 16-NOV-1998: 98WO-EP07313.  
 PF 17-NOV-1997: 97EP-0120096.  
 PR (KUFE/) KUFE P.  
 PA Borschert K, Kufer P, Luternpuese R, Raum T, Zettl F;  
 PI WPI: 1999-338004/28.  
 DR P-PSDB; Y17964.  
 XX Phase display system for identification of binding site domains  
 PT retaining capacity to bind an epitope  
 PS Disclosure: Fig 6.10; 152pp: English.  
 XX The invention relates to a method of identifying binding site domains  
 CC (BSD) that retain the capacity of binding to a predetermined epitope when  
 CC positioned C-terminal of at least one further domain in a recombinant bi-  
 CC or multivalent polypeptide. The method comprises (a) testing a panel of  
 CC BSD displayed on the surface of a biological display system as part of a  
 CC fusion protein for binding to a predetermined epitope, where the fusion  
 CC protein comprises an additional domain positioned N-terminal of the BSD  
 CC and an amino acid sequence that mediates anchoring of the fusion protein  
 CC to the surface of the display system; and (b) identifying a BSD that  
 CC binds to the predetermined epitope. The method is useful to identify bi-  
 CC or multivalent polypeptides that comprise antibody binding sites capable  
 CC of efficiently binding to the corresponding antigen. The polypeptides or  
 CC antibodies identified by the method are useful therapeutically and  
 CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody  
 CC fragments that bind independently of their position within bifunctional  
 CC single-chain fusion proteins can be isolated from combinatorial antibody  
 CC libraries using the new in vitro method. Sequences X77240-248 represent  
 CC DNA sequences encoding mouse scFv fragments.  
 XX Sequence 744 BP; 183 A; 174 C; 212 G; 175 T; 0 other;

Query Match 62.0%; Score 462.8; DB 20; Length 744;  
 Best Local Similarity 78.6%; Pred. No. 2.2e-111;  
 Matches 583; Conservative 0; Mismatches 147; Indels 12; Gaps 2;

QY 9 gctgcagagctcagagcgaactgtgtgagtgctcagtgctcaattgtccgcac 68  
 DB 12 gctcagagctcgtgagcgtgagctgtglaagcctgtggaacttcgaatacctcgcga 71  
 QY 69 agcttgcctcaacataaagcactatagcactgtgtaaacagagccttaaga 128  
 DB 72 ggcctctgataagcctcactaactagcagtggtgtaaacagagcctcgcga 131  
 QY 129 gggcctcgtgagtgatgtatattgacctcgtgagtggtgaaactgaatgccccgaa 188  
 DB 132 tggacttgatgtgattggagataattccctggaagtgtgtaatacactacaatgaga 191  
 QY 189 ctccagagcagagcagcagctgtgactgcagacacatcctccaagagcctactgacct 248  
 DB 192 gtccaaggcacaagccacactgactgcagacacatcttcgagcagacagcctatagcagt 251

QY 249 cagcagcctgacatctgagagacaacccgtctattactgttaatgcatctactatga 308  
 DB 252 cagttagcctgacatttgagactctgctctatctctgtgcaagctgaggaacgcgga 311  
 QY 309 atagcagcgtatgctcttgactactctgggccaagagacacaggtacacgtctctccag 368  
 DB 312 -----cgaactatgactactggtggccaagagacacaggtacacgtctctccag 362  
 QY 369 tggagcgtgtcaaggcggggtggtctctgacgtggtggtggtggtggtggtggtggtg 428  
 DB 363 tgggtgtgtgtctggggtggtggtggtggtggtggtggtggtggtggtggtggtggtg 422  
 QY 429 gtcccatctccctgctgctgtctcagcagagagagagagagagagagagagagagagag 488  
 DB 423 gtcccatctccctgctgctgtctcagcagagagagagagagagagagagagagagagag 482  
 QY 489 tcagagctgttcaacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 548  
 DB 483 tcagagctgttcaacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 542  
 QY 549 agggcagcttctcctaaagtctgactactggtggtggtggtggtggtggtggtggtggt 608  
 DB 543 agggcagcttctcctaaagtctgactactggtggtggtggtggtggtggtggtggtggt 602  
 QY 609 tgcctcacaagcagtgatctcgggacagattcactcaccatcagcagtgatgagc 668  
 DB 603 tgcctcacaagcagtgatctcgggacagattcactcaccatcagcagtgatgagc 662  
 QY 669 tgaagcctgagcagtttacttactcagcaaatcctata---actcagcagctggcg 725  
 DB 663 tgaagcctgagcagtttacttactcagcaaatcctata---actcagcagctggcg 722  
 QY 726 gggcaccagctcgaaatcaaa 747  
 DB 723 tgggaccagcttgagatcaaa 744

RESULT 10  
 V36236  
 ID V36236 standard; DNA: 729 BP.  
 XX V36236:  
 AC  
 XX  
 DR 08-SEP-1998 (first entry)  
 XX  
 DE DNA of scFv 421 which binds to mutant p53 proteins.  
 XX Single chain antibody; scFv 421; mouse; p53 protein; oligomerisation;  
 KW regulatory domain; p53 mutant; H273; W248; G281;  
 KW p53-dependent trans-activating activity; restoration;  
 KW tumour-suppressing activity; tumour cell; treatment;  
 KW hyper-proliferation; cancer; re-stenosis; ss.  
 XX Mus sp.  
 OS WO9818825-A1.  
 PN 07-MAY-1998.  
 PD 27-OCT-1997: 97WO-FR01921.  
 PF 29-OCT-1996: 96FR-0011176.  
 PR (RHON ) RHONE-POULENC RORER SA.  
 PA Debussche L, Biacco L;  
 PI WPI: 1998-272146/24.  
 DR P-PSDB; W60769.  
 XX Restoring p53-dependent trans-activating activity to cell containing  
 PT mutant p53 - by delivering single-chain antibody specific for the

PT mutant, particularly for treatment of tumours  
XX  
PS Claim 5; Page 31; 54pp; French.

Db 700 ttcggtgctgacccaagctggaatcaaa 729

CC The presequence encodes a single chain antibody (ScFv) designated  
CC 421. The antibody binds to an epitope present in the C-terminal region  
CC of the p53 protein that includes oligomerisation and regulatory domains,  
CC specifically between positions 320 and 393. ScFv 421 is directed against  
CC p53 mutants, particularly H273, W48 and G261 mutants. When the ScFv is  
CC introduced into cells containing a mutant p53 protein, p53-dependent  
CC trans-activating activity is restored. ScFv 421 is specific for  
CC p53-mutants that have lost tumour-suppressing activity and are present in  
CC tumour cells. It is particularly used to treat hyper-proliferation  
CC associated with these mutants (e.g. cancer and re-stenosis) but may also  
CC be used in vitro for studying mechanisms of activity of p53 or its mutant  
CC and to purify or detect p53.

SQ Sequence 729 BP; 174 A; 171 C; 207 G; 177 T; 0 other;

Query Match	61.7%	Score	460.8	DB	19	Length	729
Best Local Similarity	-79.2%	Pred	No.7.3e-111				
Matches	594	Conservative	0	Mismatches	132	Indels	24
						Gaps	3

[illegible]

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RESULT  11
T86234
XX      T86234 standard; CDNA; 749 BP.
AC      T86234;
XX
DT      24-NOV-1997 (first entry)
XX
XX      Anti-human protein p53 single chain antibody ScFv 421 CDNA fragment.
DE
XX
XX      Leucine zipper domain; LZD; oligomerisation domain; mutant; mutain;
KW      substitution; replacement; transactivation; viral protein VP16; HSV;
KW      anti-oncogene; hyperproliferation; cancer; retinosis; ScFv;
KW      tumour suppression; apoptosis; single chain antibody variable domain
KW      ss.

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Sequence 749 BP; 173 A; 179 C; 221 G; 176 T; 0 other;

Query Match	61.3%	Score 457.6	DB 18	Length 749
Best Local Similarity	78.9%	Pred. No. 5e-110		
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				Gaps 3

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2001, 01:29:16 ; Search time 2148.34 Seconds  
(without alignments)  
1509.669 Million cell updates/sec

Title: US-09-297-181-3

Perfect score: 1 caggtcaagtcgagagtc.....gcacccaagctggaatcaaa 747

Sequence: 747

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 12370408 seqs, 2170871038 residues

Total number of hits satisfying chosen parameters: 24740816

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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43: /cgn2\_6/ptodata/2/pna/US128\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	510.2	68.3	1725	18 US-09-468-029-57	Sequence 57, Appl
3	504	67.5	759	16 US-09-235-073-10	Sequence 10, Appl
4	501.6	67.1	1668	18 US-09-468-029-59	Sequence 59, Appl
5	460.8	61.7	729	16 US-09-297-181-1	Sequence 1, Appl
6	457.6	61.3	749	13 US-08-983-035-46	Sequence 46, Appl
7	457.6	61.3	1611	13 US-08-983-035-37	Sequence 37, Appl
8	452.8	60.6	768	13 US-08-930-480-4	Sequence 4, Appl
9	445.2	59.5	714	21 US-09-559-019-30	Sequence 30, Appl
10	443.6	58.7	1679	17 US-09-364-088-15	Sequence 15, Appl
11	438.4	58.7	1679	19 US-09-523-279-15	Sequence 15, Appl
12	438.4	58.7	1679	19 US-09-523-279-15	Sequence 15, Appl
13	438.4	58.7	1679	19 US-09-523-279-15	Sequence 15, Appl
14	438.4	58.7	1679	19 US-09-523-279-15	Sequence 15, Appl
15	435.4	56.8	924	15 US-09-171-025-26	Sequence 26, Appl
16	424	56.8	930	15 US-09-171-025-3	Sequence 3, Appl
17	424	56.8	930	15 US-09-171-025-3	Sequence 3, Appl
18	407	54.5	789	18 US-09-468-029-75	Sequence 75, Appl
19	397.4	53.2	728	23 US-09-656-466-26	Sequence 26, Appl
20	394.2	52.8	1518	18 US-09-445-375A-5	Sequence 5, Appl
21	394.2	52.8	2090	18 US-09-445-375A-6	Sequence 6, Appl
22	377.2	50.5	819	55 US-09-523-095A-33	Sequence 33, Appl
23	377.2	50.5	828	55 US-09-523-095A-31	Sequence 31, Appl
24	375.4	50.3	726	9 US-08-553-497-29	Sequence 29, Appl
25	375.4	50.3	2165	3 US-07-990-263-6	Sequence 6, Appl
26	375.4	50.3	2165	3 US-07-990-263-6	Sequence 6, Appl
27	373.8	50.0	756	14 US-09-000-802-10	Sequence 10, Appl
28	372.8	49.9	783	21 US-09-589-870-36	Sequence 36, Appl
29	372	49.8	753	1 PCT-US00-19643-16	Sequence 16, Appl
30	372	49.8	771	19 US-09-526-738-1	Sequence 1, Appl
31	372	49.8	780	19 US-09-526-738-3	Sequence 3, Appl
32	372	49.8	792	1 PCT-US00-19643-9	Sequence 9, Appl
33	369.4	49.5	732	9 US-08-553-497-19	Sequence 19, Appl
34	368.4	49.4	741	55 US-09-523-095A-39	Sequence 39, Appl
35	368.4	49.3	726	9 US-08-553-497-25	Sequence 25, Appl
36	366	49.0	819	55 US-09-523-095A-29	Sequence 29, Appl
37	366	49.0	828	55 US-09-523-095A-25	Sequence 25, Appl
38	364.6	48.8	732	9 US-08-553-497-21	Sequence 21, Appl
39	364	48.7	723	16 US-09-202-000-9	Sequence 9, Appl
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43	354.8	47.5	1460	7 US-07-989-846B-18	Sequence 18, Appl
44	354.8	47.5	1460	7 US-08-392-338-18	Sequence 18, Appl
45	354.8	47.5	1460	18 US-09-443-213-18	Sequence 18, Appl

#### ALIGNMENTS





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Query Match 594: 61.7%: Score 460.8: DB 16: Length 729;
Best Local Similarity 79.2%: Pred. NO. 3.6e-122;
Matches 594; Conservative 0; Mismatches 132; Indels 24; Gaps 3

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QY 121 ccttgaaagggtcctgtgagctgtgatatatgtatctccagagagctgtgaaactgaat 180
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RESULT 6
US-08-983-035-46
: Sequence 46, Application US/08983035
: GENERAL INFORMATION:
: APPLICANT: CONSEILLER, Emmanuel
: APPLICANT: BRACCO, Laurent
: TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
: TITLE OF INVENTION: P53 THEREOF
: NUMBER OF SEQUENCES: 59
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Rhone-Poulenc Rorer Inc.
: STREET: 500 Arcola Road, Maitstop 3C43
: CITY: Collegeville
: STATE: PA
: COUNTRY: USA
:

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Qy 181 gcccggaacttcacagggcgaagccactgtactgtacagacacacacacacacac 240
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Qy 241 ctgacactacagacgtcagatctgagacacacacacacacacacacacacac 300
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Db 379 CCGACTGGCGCGTACTAC-----TTTGACTACTGGGCGCAAGGACACAGGTCACCGTC 432
Qy 361 tccctcagatgagagcggttcacagcgagagtgagctcgtgagtgagacacacacac 420
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Qy 421 ctacccagctccatctccctgctgtgtacagcagagagagagagtgctatgagctgc 480
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Db 592 CAGAGGCGGAGCACTTCTCCAAACTGTGATTATAGCAACATCCAACTGGCTTGGA 651
Qy 601 gtccctgatacgtctcacaagcagtgatctgtgacagatcttcaactcaccacacacag 660
Db 652 GTCCCTGCTCGCTTCACTAGTGGCAGTGTGATCTGGACCTCTTACTCTCTCAATCAACCCGA 711
Qy 661 gtgcagcagcagacacctgtgacatttacttgaagcaaa---tctataatcaccagag 717
Db 712 ATGAGAGCGTAAGATGCTCCACTTTACTGCGACGAAGAAGATGATGATGATGATGAT 771
Qy 718 ttcgagcgagggcagcagcagctggaatacaaa 747
Db 772 TTCGGTGTGGCAGCAAGCTGTGAGCTGAAA 801

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RESULT 2  
US-08-661-052-15  
Sequence 15, Application US/08661052  
Patent No. 5837243

## GENERAL INFORMATION:

APPLICANT: Yashwant M. Deo  
APPLICANT: Joel Goldstein  
APPLICANT: Robert Graziano  
APPLICANT: Chezian Somasundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISD  
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16

## CORRESPONDENCE ADDRESS:

ADDRESS: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts

## COUNTRY: USA

ZIP: 02109-1875

## COMPUTER READABLE FORM:

MEDIA TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/661,052
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1679 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 11..1667
US-08-661-052-15

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Query Match 58.7%; Score 438.4; DB 2; Length 1679;  
Best Local Similarity 77.7%; Pred. No. 4.5e-115;  
Matches 580; Conservative 0; Mismatches 136; Indels 30; Gaps 3;

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Qy 5 tcaagctcagagagctcagggcagagactgtgagtgacagggccctcagatcattgtctc 64
Db 843 TCAAACTTCAGAGAGCTGTGGGCGAGACTTGTAGGCTCAGGAGCCCTCAATCAAGTGTCTT 902
Qy 65 gacagcttcaggctcacaactaaagactactatgacactgagtgagaaagagcctg 124
Db 903 GCACAGCTTCAGCTTCAACATTAAAGACTCTTATATGACTGTGAGCGAGGCGCTG 962
Qy 125 aagaagccttgagtgatgatatgatactcctgagagtgagtgaaatgaaatgccc 184
Db 963 AACAGGCGCTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1022
Qy 185 cgaacttcagagggcagagccactgtgactgcagaaactctcacaacacacacacac 244
Db 1023 CGAAGTTCAGAGGCAAGGCACTTTTACTACAGACACATCTCTCAACACACCTTACCTGC 1082
Qy 245 acccagagcctgacatctgagacacacacacacacacacacacacacacacacacac 304
Db 1083 AGCTAGCAGCCTGACATCTGAGGACACTGCCGTATTATTATGATGAGGAGACTCCGA 1142
Qy 305 atgaatacgaagcgtatgtcttgactactgtgggccaagggacacacacacacacac 364
Db 1143 CTGGGCGCTACTAC-----TTTGACTACTGGGCGCAAGGACACCGGCTACCGTCTCT 1196
Qy 365 caggtgagagcggttcagcgagagtggtctgtgcggtgagcgagatcggaacttgagctca 424
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Qy 425 cccagctccacatctccctgctgtgtcagcagagagagagtgagcgtatgagcacaat 484
Db 1257 CCGAGTCTCCAGCAATCATGTCTGCACTCTCCAGGGGAGAAAGTCAACCTGCACTG 1316
Qy 485 ccagtcagagctgttcaacagtagaacccgaagaatcactgtgctgtgatacagaga 544
Db 1317 COAGCTCAAGTGT-----AAGTTACTATGACACTGTTCAGAGCA 1355
Qy 545 aaccagggcagctctcctaaagtgtgatactactgtgacacacacacacacacacacac 604
Db 1356 AGCCAGGCACTTCTCCAAACTGTGATTATAGCAACATCCAACTGCTTGTGAGTCC 1415
Qy 605 ctgacagcttcacagcagtgatctgagacagatcttcaactcaccacacacagcagtgag 664
Db 1416 CTGCTGCTTCAAGTGGCAGTGTGATCTGGGACCTTACTCTCTCAATCAATCAAGCGAATG 1475

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QY 593 aatctgagtccttcgacgccttcacagcagctgagatctgggacagatttcacacac 652  
 DB 1794 AATCTGGGGCCCTGATCGCTTACAGGAGCTGATCTGGACAGATTCTCCTCCA 1853  
 QY 653 tcagcagctgctcagcagctgagacctgagcttattactgacgaactctata---atc 709  
 DB 1854 TCAGCAGTGTGAAGACTGAGACCTGGCAGTTATTACTGTCTCAGAGTATTATAGCTATC 1913  
 QY 710 taccgaccttcgagcggggcaccacagctggaatcaa 746  
 DB 1914 CCTCAGCTTCGGTCTGCGGACCAAGCTGCTTAA 1950  
 RESULT 7  
 US-08-553-497A-19  
 ; Sequence 19, Application US/08553497A  
 ; Patent No. 5844093  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KETTLEBOROUGH, C. A.  
 ; APPLICANT: BENDIG, MARY M.  
 ; APPLICANT: ANSELL, KEITH H.  
 ; APPLICANT: GUSNOW, DETLEF  
 ; APPLICANT: ADAN, JAUME  
 ; APPLICANT: MITJANS, FRANCESC  
 ; APPLICANT: ROSELL, ELISABET  
 ; APPLICANT: BLASCO, FRANCESC  
 ; APPLICANT: PIULATS, JAUME  
 ; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR  
 ; TITLE OF INVENTION: ANTIBODIES  
 ; NUMBER OF SEQUENCES: 30  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MILEN, WHITE, ZELANO & BRANIGAN, P. C.  
 ; STREET: 2200 CLARENDON BLVD. SUITE 1400  
 ; CITY: ARLINGTON  
 ; STATE: VA  
 ; COUNTRY: US  
 ; ZIP: 22201  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/553,497A  
 ; FILING DATE: 17-NOV-1995  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: WO PCT/EP95/00978  
 ; FILING DATE: 16-MAR-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: EP 94104160.0  
 ; FILING DATE: 17-MAR-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: EP 94118970.6  
 ; FILING DATE: 02-DEC-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: HAMLET-KING, DIANA  
 ; REGISTRATION NUMBER: 33,302  
 ; REFERENCE/DOCKET NUMBER: MERCK 1726  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 703-243-6333  
 ; TELEFAX: 703-243-6410  
 ; INFORMATION FOR SEQ ID NO: 19:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 732 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHEICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:

; ORGANISM: mouse  
 ; STRAIN: Balb/c  
 ; TISSUE TYPE: splenocytes  
 ; IMMEDIATE SOURCE:  
 ; CLONE: 10 D 2 (single-chain Fv, heavy and light  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..732  
 ; US-08-553-497A-19  
 Query Match 49.5%; Score 369.4; DB 2; Length 732;  
 Best Local Similarity 71.7%; Pred. No. 1.1e-95;  
 Matches 541; Conservative 0; Mismatches 181; Indels 33; Gaps 3;  
 QY 2 aggtcaagcttcagagagtaggagcagaactgtgagtcagggcctcagcaattgt 61  
 DB 2 AGGTGACGCTGACGACGCTGTTGGGCTGAAGCTGTGAAGCTGGGCTTACGTGAAGTTGT 61  
 QY 62 cctgcacagcttcgtctcaacattaaagactatatactgacgttggtgaacagagc 121  
 DB 62 CCTGCAAGGCTTCGCGCTACACTTCACCAGCCACTGATGACACTGGTGTGAAGCAGAGG 121  
 QY 122 ctgaagaggccttgagtgattgatatatactctcgtgaggtggtgaactgaatg 181  
 DB 122 CTGAGCAAGGCTTGAGTGATCGGAGAGTTTAATCCAGCAAGGCGCTACTACTACA 181  
 QY 182 ccccgacacttcagagcaagggcactgtgactgcagacacatctcccaacagactac 241  
 DB 182 ATGAGAAATTCAGAGCAAGGCGCACACTGACTGTAGACAAATCTCCACACAGCTTACA 241  
 QY 242 tgcacctcagcagcctgacatctgagagacacaacgcgtctatcagtaagtcagtc 301  
 DB 242 TGCACTCAGCAGCGCTGACATCTGAGAGACTCGCGTCTATTACG---TGCAAGTCGGG 298  
 QY 302 actatgaatacagagcgtatgcttggactactggggccaaggaaccagcgtccgtct 361  
 DB 299 ACTATGATTAACGACGAGCGAGTGTGACTACTGGGCGCAAGGACACGCTCACCGTCT 358  
 QY 362 cctcaggtgagagcggttcagcggaggtgctcgtggcggtggagatcgacattggc 421  
 DB 359 CCTCAGGTGGCGGTGCTGGCGGCGGTGGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCG 418  
 QY 422 tcaccagctcctcattctccctggtgtgtcagcagagaggaaggctgctatgaactgca 481  
 DB 419 TCACCAGCTCTCAGCAATCATGTCTGATCTCCAGGGGAGAGGTCAACCATGACTGCA 478  
 QY 482 aatcagtcagagctgttcaacagtagaaccggaagaattactgtgtgtcagc 541  
 DB 479 GTGCCAGCTCAAGTGT-----AAGTTACATGTACTGTGTAACAC 517  
 QY 542 agaaaccagggcagctctcctaagtgtgattctactgtggcaccctcctggagatctgg 601  
 DB 518 AAAAAACAGAGATCTCCGCCAGACTCTGATTTATGACACATCAACCTGCGTTGTGGG 577  
 QY 602 tccctgagcttcacagcagtgatctgggacagattcactcaccacagcagtg 661  
 DB 578 TCCCTGTTGCTTACGTGAGTGGGTGCTGGGACCTCTTACTCTCTCAATCAGCCGGA 637  
 QY 662 tgcaggtcgaagaccttgcagttatattactgcaagaactctataatctacc----- 713  
 DB 638 TGGAGGCTGAAGATGCTGCACTTATTACTGCGACAGAGTGAGTGTATACCAACCATCATGT 697  
 QY 714 -gaagttggcgggggcaccgaagctggaaatcaa 747  
 DB 698 ACACGTTGGAAGGGGAGCAAGCTGGAATTA 732  
 RESULT 8  
 US-08-553-497A-25  
 ; Sequence 25, Application US/08553497A  
 ; Patent No. 5844093

```

1 GENERAL INFORMATION:
2 APPLICANT: KETTLERBOROUGH, C. A.
3 APPLICANT: BENDIG, MARY M.
4 APPLICANT: ANSELL, KEITH H.
5 APPLICANT: GUSSOW, DETLEF
6 APPLICANT: ADAM, JAUME
7 APPLICANT: MITTANS, FRANCESCA
8 APPLICANT: ROSELL, ELISABET
9 APPLICANT: BLASCO, FRANCESC
10 APPLICANT: PUJOLTS, JAUME
11 TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
12 TITLE OF INVENTION: ANTIBODIES
13 NUMBER OF SEQUENCES: 30
14 CORRESPONDENCE ADDRESS:
15 ADDRESSEE: MILLER, WHITE, ZELANO & BRANNIGAN, P.C.
16 STREET: 2200 CLARENDON BLVD. SUITE 1400
17 CITY: ARLINGTON
18 STATE: VA
19 COUNTRY: US
20 ZIP: 22201
21
22 COMPUTER READABLE FORM:
23 MEDIUM TYPE: Floppy disk
24 COMPUTER: IBM PC compatible
25 OPERATING SYSTEM: PC-DOS/MS-DOS
26 SOFTWARE: PatentIn Release #1.0, Version #1.30
27 CURRENT APPLICATION DATA:
28 APPLICATION NUMBER: US/08/553,497A
29 FILING DATE: 17-NOV-1995
30 CLASSIFICATION: 530
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: WO PCT/EP95/00978
33 FILING DATE: 16-MAR-1995
34 PRIOR APPLICATION DATA:
35 APPLICATION NUMBER: EP 94104160.0
36 FILING DATE: 17-MAR-1994
37 PRIOR APPLICATION DATA:
38 APPLICATION NUMBER: EP 94118970.6
39 FILING DATE: 02-DEC-1994
40 ATTORNEY/AGENT INFORMATION:
41 NAME: HAMLET-KING, DIANA
42 REGISTRATION NUMBER: 33,302
43 REFERENCE/DOCKET NUMBER: MERCK 1726
44 TELECOMMUNICATION INFORMATION:
45 TELEPHONE: 703-243-6333
46 TELEFAX: 703-243-6410
47 INFORMATION FOR SEQ ID NO: 25:
48 SEQUENCE CHARACTERISTICS:
49 LENGTH: 726 base pairs
50 TYPE: nucleic acid
51 STRANDEDNESS: single
52 TOPOLOGY: linear
53 MOLECULE TYPE: cDNA
54 HYPOTHEetical: NO
55 ANTI-SENSE: NO
56 FRAGMENT TYPE: N-terminal
57 ORIGINAL SOURCE:
58 ORGANISM: mouse
59 STRAIN: Balb/c
60 TISSUE TYPE: splenocytes
61 IMMEDIATE SOURCE:
62 CLONE: 5 F.1 (single-chain Fv, heavy, light chain,
63 CLONE: linker)
64 FEATURE:
65 NAME/KEY: CDS
66 LOCATION: 1..726
67
68 US-08-553-497A-25
69
70 Query Match 49.3%; Score 368.4; DB 2; Length 726;
71 Best Local Similarity 71.6%; Pred. No. 2.2e-95;
72 Matches 537; Conservative 0; Mismatches 186; Indels 27; Gaps 3

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[illegible]

STATE: VA  
COUNTRY: US  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,497A  
FILING DATE: 17-NOV-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/00978  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94104160.0  
FILING DATE: 17-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94118970.6  
FILING DATE: 02-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: HAMLET-KING, DIANA  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: MERCK 1726  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 732 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
-HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: mouse  
STRAIN: Balb/c  
TISSUE TYPE: splenocytes  
IMMEDIATE SOURCE:  
CLONE: 3 D 3 (single-chain Fv, heavy and light chain  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..732  
US-08-553-497A-21

	Query Match	Similarity	48.8%	Score 364.6	DB 2:	Length 732:
	Best Local	Similarity	71.3%	Pred. No. 2.6e-94:		
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Db	2	AGGTCCAACTCAGCAGTCAGGCGGGTGAAGTGTGAAGCTGGGGCTTCAGTCAATTGT	61			
QY	62	cctgcacagcttccttgcgtccaacattaagaactactatatgcactgygtgtgaacagagcc	121			
Db	62	CCTGCAAGGCTTCCCGGCTACACTTCACCAGGCACATGGATGACCTGGTGGAAGCAAGGG	121			
QY	122	ctgaagaggggccttgtagtgcattgatataatcatctgcagtgcaggtgtgtgaacctaagtaagc	181			
Db	122	CTGCAACAAGGCTTTAGTGTGATCGGAGATTTAATCCAGCAAAGGCCCTTAATAATTACA	181			
QY	182	cccccaactctccaggggcgaagggccactgtgtactgcagagacacatcctccaacacagcctacc	241			
Db	*182	ATGAAATAATCATAGAAGCAAGGCCACACCTACTCTGTAACAAATCTCTCACACAGCCTTACA	241			
QY	242	tgcacctcagcacagctgnacatcttgaggacacaacgcgttttatctactgttaatgcagtcattct	301			

Db	242	TGCACATCAGCAGCCCTACACATCTGAGGACCTCGGCTCATTTACTG---TGCCAGTCGGG	298
QY	302	actaagaatcagaagcgtatgcttggactactcgggccaaggagccacggtacccgtc	361
Db	299	ACTATGATTATGAGAGGACGGCTACTTTGACTACTGGGCCAAGGACCCAGCTTACCCTCT	358
QY	362	cctaagatlgtaggcggttcacgaggaaagtgcgtcggatggcgcgagatcgcgacattgagc	421
Db	359	CCCTAGGAGGGGGGAGGCTCGGGCGGTGGTGGGTCGGGCGGATCTGCATTTGAGC	418
QY	422	tcacccagcttcacatcttcctcgtgctgtgcagcaggaagaaagtgcctatagctgcga	481
Db	419	TCACCCAGCTCCCAACATATCATGCTTCATCTCCAGGGGGAAGGTACCATATACCTGCA	478
QY	482	aatccatcagagtcgtcttcaacagtagaacccgaaagaattactcgtctgtgtatcagc	541
Db	479	GTGACAGCTCAAGCT-----AAGTTACATGTACTGGTACACG	517
QY	542	agaaacaacaggtcagtcctccctaagaigtctgatatctactgtggcattccactaaggaaatctggag	601
Db	518	AGAAAGACAGGATCTCTCCCCAGACTCTCTGATTATGACACATCTCAACCTGGCTTCGGAG	577
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Db	578	TCCCTGTTCCGTTTACGTAGTGGCAGTGGCTGTGGACCTTTACTCTTCACATTAAGCCGA	637
QY	662	tgacagctgaugacctcggcagtttattactgcagaagcaatcttbaatctac-----	713
Db	638	TGGAGGCTGAGAGTGCCTCACTTATACGCCAGCGAGTGGAGTAGTTACCCACCATGT	697
QY	714	-gacgttcggcgggggacacaagcttgaaatctaa	747
Db	698	ACACGTTTCGGAGGGGACCAACAGCTGAAATTAANA	732

US-08-553-497A-27  
Sequence 27, Application US/08553497A  
Patent No. 5844093  
GENERAL INFORMATION:  
APPLICANT: KETLEBOROUGH, C. A.  
APPLICANT: BENDIG, MARY M.  
APPLICANT: ANSELL, KEITH H.  
APPLICANT: GUSSEW, DETLEF  
APPLICANT: ADAM, JAUME  
APPLICANT: MITTANS, FRANCES  
APPLICANT: ROSELL, ELISABET  
APPLICANT: BLASCO, FRANCESC  
APPLICANT: PUJATS, JAUME  
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR  
TITLE OF INVENTION: ANTIBODIES  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
STREET: 2200 CLARENDON BLVD. SUITE 1400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: US  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,497A  
FILING DATE: 17-NOV-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NO PCT/EP95/00978  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94104160.0

FILING DATE: 17-MAR-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 94118970.6  
 FILING DATE: 02-DEC-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HAMELET-KING, DIANA  
 REGISTRATION NUMBER: 33,302  
 REFERENCE/DOCKET NUMBER: MERCK 1726  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-243-6333  
 TELEFAX: 703-243-6410  
 INFORMATION FOR SEQ ID NO: 27:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 726 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE:  
 ORGANISM: mouse  
 STRAIN: Balb/c  
 TISSUE TYPE: splenocytes  
 IMMEDIATE SOURCE:  
 LIBRARY: 7 G 1 (single-chain Fv, heavy, light chain,  
 LIBRARY: linker)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..726  
 US-08-553-497A-27

Query Match 47.9%; Score 357.8; DB 2; Length 726;  
 Best Local Similarity 70.8%; Pred. No. 2.2e-92;  
 Matches 530; Conservative 0; Mismatches 192; Indels 27; Gaps 3;

QY 2 aggtcaagctgcagggagtcagggcaggaactgtgaggtcaggtcaggtcgaatttgc 61  
 DB 2 AGGTCAAGCTGCAGGGAGTCAGGGGCTGAACTGTGAAGCTGGGGCTTCAGTAAGTTG 61  
 QY 62 ccgtgcacagcttcgtctcaacatlaaagactatataatgcactggtgtaaacagagc 121  
 DB 62 CCGTGCACAGCTTCGCTCACTTCAACCAAGCACTTGATCACTGGGTGAACAGAGGG 121  
 QY 122 ctgaagaaggctgtgagtgatgatatatcctcctgagagtggtgaaactgatatg 181  
 DB 122 GCTGCAAGGCTTGTGATGATCGACAGTTTATCCACAGCAAGGCGCTACTACTACA 181  
 QY 182 ccccgaaattccagggcagggcagctgtgactgcagacatactctcaaacagagcctacc 241  
 DB 182 ATGAGAAATTCAAGCAAGGCCACACTGACTGTAGCAAAATCCTCCAGACAGCTTACA 241  
 QY 242 tgcacctcagcaactgcagacatctgagagcaaacacgtcttaactgtaatgcagctatc 301  
 DB 242 TCGAAGTCAAGCAAGCTGAGACTCTGAGAGACTGCTGGGTCTATTACTG---TGCAGTCGGG 301  
 QY 302 actatgaatacgaagcgtactgtcttgactactggtggtccaaaggagcaacggtcactc 361  
 DB 299 ACTATGATTACGACGAGCGGCTACTTGTGACTACTGAGGCGCCAAAGGAGACACACGCTCT 361  
 QY 362 cctcgaagtgagggcgttcaagggtggtggtcgtggtggtggtggtggtggtggtggtggt 421  
 DB 359 CCTCAGGTGGGTGCTCGGGGCTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 421  
 QY 422 tcaaccagctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 481  
 DB 419 TCACCCAGTCTCAACAATATGTCTGCAATCTCAGGGGAGAGGTCACCATACCTGCA 478  
 QY 482 aatcagagtcagagtcgttcaacagtagaacccgaagaatactcgtggtggtggtggtggt 541  
 DB 479 GTGACAGCTCAACTGT-----AACTTACAGTGTACTGCTGACAGC 517

QY 542 aagaaccagggagctcctcctaaagtctgactcactggtggtcaccactaaggaaatcgtgag 601  
 DB 518 AGAAGACAGAGATCCTCCCAAGACTCTGATTATTAACACATCCACACCTGCTTGAGAG 577  
 QY 602 tccctgactcgttcacagagcagtgatctcgtggaacagattcactcaccatcagcagtg 661  
 DB 578 TCCCTGCTTCAAGTCAAGTGGAGTGGGTGAGACCTTACTCTCTCACAAATCAGCCGAA 637  
 QY 662 tgcagctgaagacccgtgaggttattactgcaagaaatctataatcaccg---agct 718  
 DB 638 TGGAGGCTGAAGATGCTGCTACTTATTACTGCCAGCAGTGAAGTAACTTACCCGCTCAGT 697  
 QY 719 tcggcggggcccacagctcgaatcaaa 747  
 DB 698 TCGCTGCTGGACCAAGCTGGAATATAA 726

RESULT 11  
 US-08-392-338A-18  
 Sequence 18, Application US/08392338A  
 Patent No. 5869620  
 GENERAL INFORMATION:  
 APPLICANT: Whitlow, Marc  
 APPLICANT: Wood, James F.  
 APPLICANT: Hardman, Karl  
 APPLICANT: Bird, Robert  
 APPLICANT: Filpula, David  
 TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
 STREET: 1100 New York Avenue, NW  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/392,338A  
 FILING DATE: 22-FEB-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/989,846  
 FILING DATE: 20-NOV-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/796,936  
 FILING DATE: 25-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Goldstein, Jorge A.  
 REGISTRATION NUMBER: 29,021  
 REFERENCE/DOCKET NUMBER: 0977.0030007  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2540  
 INFORMATION FOR SEQ ID NO: 18:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1460 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: both  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..1449  
 US-08-392-338A-18

Query Match 47.5%; Score 354.8; DB 2; Length 1460;  
 Best Local Similarity 71.9%; Pred. No. 1.9e-91;

Matches 539; Conservative 0; Mismatches 142; Indels 69; Gaps 3;

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QY 1 caggtcaagctgcagagtcagagcagactgtgagtcagagcctcagtcatttg 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 382 CAGGTTAGCTGCAGAGTGTGAGCTGAGTGTGAAGTGAACCTGGGCTTCAGTAAGATT 441
QY 61 tcttcagagcttctgcttcacattaaagactatatactgacgtgtgaaacagagg 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 442 TCTGCAAGGCTTCTGCTACACCTTACAGCATGACCAATTCAGTGGGGAACAGAAC 501
QY 121 cctgaagagggcctgagtgattgatatattatctctgagagtggtgaacagatat 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 502 CCTGAACAGGCGCTGGATGGATGATTTCTCCCGAAATGATTTTAATAC 561
QY 181 gccccgaacttcagagcagagccacagtgtgactcagacacatcctccacacagctac 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 562 AATGAGAGGTTCAAGGCGCAAGCCACACTGACTGACACAAATCTCCAGACAGCCCTAC 621
QY 241 ctgacactcagcagctgacatctgagagacacacgcctattactgttaatgcagtcac 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 622 GTGAGCTCAACAGCTGACATCTGAGAGATTCTGCACTGATTTCTGTACAAAGATCCCTG 681
QY 301 tactatgataagcagcgtatgcttctgactactgagggccaagggaccaggttaccgttc 360
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Db 682 AA-----TATGGCCTACTGGGGTCAAGGAACCTGACGACCGTC 720
QY 361 tctcagagtgagcggttcagcgagaggtgagctctgscgtgagtcagacattgag 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 721 TCTCTCA-----GACGTGCTG 735
QY 421 ctacaccagttccatcttccctgctgtgtcagcagagagagagtcgctatgagctgc 480
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 736 ATGTCAAGCTCCATCTCCCTCCTACCTGTGCACTGTGCGAGAGGTTACTTTGAGCTGC 795
QY 481 aaatccagtcagagtcgtctcaacagtagaacccgaagaattactggttgattacag 540
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 796 AAGTCAGTAGAGCTTTTATATAGTGTAATCAAAAGAACTAGTGGCTGGTACAG 855
QY 541 cagaaccagagcagctcctctaaagtctgatactactgagcattcagtaggaatctgga 600
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 856 CAGAAACAGGCGAGTCTCTAAACTGATTTACTGGGCGATCCGTAAGGAATCGGG 915
QY 601 gtccctgactgcttcacagcagtgagctcagagcagattcactcctacacatcagcagt 660
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 916 GTCCCTGATGCTTACAGCAGCAGATGCGACAGATTTCACTCTCCATCAGCAGT 975
QY 661 gtgcagcgtgaagaccctgagctgttattactgcaagaactctata---atccacgagc 717
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Db 976 GTGAAGACTGAAGACTGAGATTTATTACTGTGCAAGATATTATAGCTATCCCTCAGC 1035
QY 718 ttcgagcgagggcaccagcctggaatcaaa 747
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1036 TTGCGTCTGGGACCAAGCTTTGTCTGAAA 1065
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## RESULT 12

US-09-166-750-18  
; Sequence 18, Application US/09166750  
; Patent No 6025165

## GENERAL INFORMATION:

APPLICANT: Whitlow, Marc  
APPLICANT: Wood, James F.  
APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert  
APPLICANT: Filpula, David  
APPLICANT: Rolence, Michelle  
TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW  
CITY: Washington

STATE: D.C.  
COUNTRY: U.S.A.

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/166,750  
FILING DATE: Herewith

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/392,338  
FILING DATE: 22-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:

NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.003000C

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540

INFORMATION FOR SEQ. ID NO: 18:

## SEQUENCE CHARACTERISTICS:

LENGTH: 1460 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both

## FEATURES:

NAME/KEY: CDS  
LOCATION: 1..1449

US-09-166-750-18

Query Match 47.5%; Score 354.8; DB 3; Length 1460;  
Best Local Similarity 71.9%; Pred. No. 1,9e-91;

Matches 539; Conservative 0; Mismatches 142; Indels 69; Gaps 3;

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QY 1 caggtcaagctgcagagtcagagcagactgtgagtcagagcctcagtcatttg 60
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Db 382 CAGGTTAGCTGCAGAGTGTGAGCTGAGTGTGAAGTGAACCTGGGCTTCAGTAAGATT 441
QY 61 tcttcagagcttctgcttcacattaaagactatatactgacgtgtgaaacagagg 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 442 TCTGCAAGGCTTCTGCTACACCTTACAGCATGACCAATTCAGTGGGGAACAGAAC 501
QY 121 cctgaagagggcctgagtgattgatatattatctctgagagtggtgaacagatat 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 502 CCTGAACAGGCGCTGGATGGATGATTTCTCCCGAAATGATTTTAATAC 561
QY 181 gccccgaacttcagagcagagccacagtgtgactcagacacatcctccacacagctac 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 562 AATGAGAGGTTCAAGGCGCAAGCCACACTGACTGACACAAATCTCCAGACAGCCCTAC 621
QY 241 ctgacactcagcagctgacatctgagagacacacgcctattactgttaatgcagtcac 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 622 GTGAGCTCAACAGCTGACATCTGAGAGATTCTGCACTGATTTCTGTACAAAGATCCCTG 681
QY 301 tactatgataagcagcgtatgcttctgactactgagggccaagggaccaggttaccgttc 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 682 AA-----TATGGCCTACTGGGGTCAAGGAACCTGACGACCGTC 720
QY 361 tctcagagtgagcggttcagcgagaggtgagctctgscgtgagtcagacattgag 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 721 TCTCTCA-----GACGTGCTG 735
QY 421 ctacaccagttccatcttccctgctgtgtcagcagagagagagtcgctatgagctgc 480
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; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1449
US-09-166-093-18

Query Match      47.5%; Score 354.8; DB 3: Length 1460;
Best Local Similarity 71.9%; Pred No. 1.9e-91;
Matches 539; Conservative 0; Mismatches 142; Indels 69; Gaps 3;

Db 736 ATGTCACAGTCTCCATCCCTACCTGTGTCTGCTGAGGAGGTTACTTGTACCTGC 795
QY 481 aatlcagcagaggtctgttcaacagtagaacccgaagaattactgtgttgatcag 540
Db 796 AAGTCCAGTCAGAGCCTTTATATATAGTGGTAATCAAAAGAACTTGGCTGGTCCAG 855
QY 541 cagaaccagggagctctcctaagtgctgtatctactgtggtcctcctcaaggaaatcgtga 600
Db 856 CAGAAACGAGGAGGAGTCTCTTAACGTCTATTTACTGGGCACTCCGTAGGAATCTGGG 915
QY 601 gtccctgattcgtctcaagcagtgatctctggacagattcactcctcaccatcagcagt 660
Db 916 GTCCCTGATCGCTTCAACAGGAGCTGATCTGGACAGATTTCACCTCTCCATCAGCAGT 975
QY 661 gtccagcgtgaagactcgtgaggtttattactgaagcaatctata---atccacgagc 717
Db 976 GTGAAGACTGAAGACCTGGAGTTTATTTACTGTGACGACGATATTATAGCTATCCCTCAG 1035
QY 718 ttcgagcgaggccacaaagctggaatcaaa 747
Db 1036 TTGCGTGTGGGACCAAGCTTGTGCTGAAA 1065

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RESULT 13
US-09-166-093-18
; Sequence 18, Application US/09166093
; Patent No. 6027725
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Rolence, Michelle
; APPLICANT: Rolence, Michelle
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,093
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.003000B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ. ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1460 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1449
US-09-166-093-18

Query Match      47.5%; Score 354.8; DB 3: Length 1460;
Best Local Similarity 71.9%; Pred No. 1.9e-91;
Matches 539; Conservative 0; Mismatches 142; Indels 69; Gaps 3;

QY 1 cagtgaaagctcagagagtcagagagagagagagagagagagagagagagagagagagagagag 60
Db 382 CAGGTTCAGCTGAGCAGAGCTGACGCTGAGTGGTAAACCTGGGGCTTCAGTGAAGATT 441
QY 61 tectcagcagctctgtgtctcaacatlaaagactatgatcactgtgtgtgaacagag 120
Db 442 TCCTGCAGGCTTCTGCTACACCTTCACTGACCAATTCATTCACCTGCTGGAACGAAAC 501
QY 121 cctgaagagggcctgagtgatgatatattgatcctcgaagagtgatgaactgatat 180
Db 502 CCGAAACAGGGCTGGAATGATGATTTTCTCCGGAATATATATTTTAAATAC 561
QY 181 gccccgaacttcagagcagagccactgtgactgcagacacacccctcaacacagcctac 240
Db 562 AATGAGAGGTTCAGAGGCAAGGCACTGACGACAGACAAATCCCTCAGACTGCTAC 621
QY 241 ctgacactaagcagctgacatctgagacacacccgtctatctgtatgacagtcac 300
Db 622 GTGACAGCTCAACAGCCTGACATCTGAGATCTGCACTGTATTTCTGCAAGATCCCTG 681
QY 301 tactatgaatgaagcagcgtatgcttgagactcctgagcagagagagagagagagagag 360
Db 682 AA-----TATGGCTTACTGGGCTCAAGAACTCAGTACCTGC 720
QY 361 tctcagagtgagcggttcagcgagaggttgctcgtggtgagcagacatgag 420
Db 721 TCCTCA-----GACGTCGTG 735
QY 421 ctcaaccagcttcacatctccctgtgtgtgcaagcagagagagagagcgtatgagctgc 480
Db 736 ATGTCACAGTCTCCATCCCTACCTGTGTGAGTGGGAGAGAGCTTACTTGTGACCTGC 795
QY 481 aatlcagcagaggtctgttcaacagtagaacccgaagaattactgtgtgtatcag 540
Db 796 AAGTCCAGTCAGAGCCTTTATATATAGTGGTAATCAAAAGAACTTGGCTGGTCCAG 855
QY 541 cagaaccagggagctctcctaagtgctgtatctactgtggtcctcctcagagagatcgtga 600
Db 856 CAGAAACGAGGAGGAGTCTCTTAACGTCTATTTACTGGGCACTCCGTAGGAATCTGGG 915
QY 601 gtccctgattcgtctcaagcagtgatctctggacagattcactcctcaccatcagcagt 660
Db 916 GTCCCTGATCGCTTCAACAGGAGCTGATCTGGACAGATTTCACCTCTCCATCAGCAGT 975
QY 661 gtccagcgtgaagactcgtgaggtttattactgaagcaatctata---atccacgagc 717
Db 976 GTGAAGACTGAAGACCTGGAGTTTATTTACTGTGACGACGATATTATAGCTATCCCTCAG 1035
QY 718 ttcgagcgaggccacaaagctggaatcaaa 747
Db 1036 TTGCGTGTGGGACCAAGCTTGTGCTGAAA 1065

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RESULT 14
US-09-172-019-18
; Sequence 18, Application US/09172019
; Patent No. 6103889
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert

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Search completed: February 17, 2001, 22:59:28  
Job time: 35119 sec

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? REFERENCE/DOCKET NUMBER: 0977.003000A
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 371-2600
? TELEFAX: (202) 371-2540
? INFORMATION FOR SEQ ID NO: 18:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1460 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: both
? TOPOLOGY: both
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1449
? US-09-166-094-18

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Query Match	47.5%	Score 354.8;	DB 3;	Length 1460;
Best Local Similarity	71.9%;	Pred. No. 1.9e-91;		
Matches 539;	Conservative 0;	Mismatches 142;	Indels 69;	Gaps 3

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Db	382	CAGGCTTCAGCTGCACGACGCTGACGCTGCAATTTGGTGAACCTGGGGCTTCAGTGAAATTT	441
OY	61	tccctgcacagctcttcgtgcttcaacattaaagactactatatacgacctgggttgaaacagag	120
Db	442	TCCTGCAGAGGCTTGTGGCTACCTTCACAGACCAATTCAGTGGGTGAACAAGAAC	501
OY	121	ccctgaagagggccttgcagtgagtgattgatatattgacctgcagagtggtgtyaaactgaatat	180
Db	502	CCTGACACGGGGCCTGGATGGATGGATATTTTTCGCCGAATGATGATTTTAAATAC	561
OY	181	gcccgcgaactctcagggcagaagggccactgctacgcgagaaatccctccaaacagctctac	240
Db	562	AATGAGAGGTTCAAAGGGCCAAAGGCCACACTACATGCAGACAAATCCCTCCAGCACTGGCTTAC	621
OY	241	ctgcacccctcagcagcctgcgacatctgcgagagacacaaacgctctattactgtaatgcagctac	300
Db	622	GTGCAGGCTCAACACGCTCGACATCGAGAGATTTCGACAGTATTTTCGTACAGATGCCG	681
OY	301	tactatgaatacgaagcgtactgcttgcgactctggggccaaagacacggtcactgcgtc	360
Db	682	AA-----TATGGCTACTGGGGTCAAGGAACCTCAGTACGCCGC	720
OY	361	tcctcagtgtagggcgtgtcgaaggggaggggctctggcggtgtagcagtcgaactttag	420
Db	721	TTCTCTCA-----GACGTCGGT	735
OY	421	ctcaccacagcttcacatctccctgcgtgctgtctcagcagagagaaggtctcgatagcgtc	480
Db	736	ATGTACAGGTCTCATCTCTCCCTACCTGTCAGTTGCGCAGAAAGGTTACTTTGACACTGC	795
OY	481	aaatccagctcagagtcgtgtccaacagtagaaccgcgaagaagaattacttgctggtatcag	540
Db	796	AAGTCCATCTAGACCCCTTTATATAGGTGTAAACCAAAAGAACACTTGGCCGTGTACACAG	855
OY	541	cagaaaccagggcggttccctaaagtgctgatatctactgcggcaccctcagtggaatctgga	600
Db	856	CAGAAACCAAGGGCAGGTCTCTTAACTCTATTTACTGGGCAATCCCTGAGGGAGATTTGGG	915
OY	601	gtccctgtatcgtcttcacagcgaagtgagatctgcggacagattactactcctcaacatcaagcgt	660
Db	916	GTCCCTGATCCCTTCACAGGCAAGTGGATTCGGGACAGATTTCACTCTCTCCATCAGCAAT	975
OY	661	gtgcagagctgaagacctgcagagttattactctgcaagcaatcttata--atctaccagag	717
Db	976	GTGAAGACTGAAGACCTGGGCGAGTTTATTACTGTCAGCAGATATATATAGCATATCCCTCCACAG	1033
OY	718	ttcggcggygggcaccagagctbgyaatcaaa	747
Db	1036	TTTCGGTGTGGGACCAAGCTTGTGCTCAAA	1065

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 17, 2001, 13:13:59 ; Search time 1856.43 seconds  
(without alignments)  
2009.685 Million cell updates/sec

Title: US-09-297-181-1

Perfect score: 729

Sequence: 1 caggtgcagctgcagcagtc.....gcaccaagctcgaatcaaa 729

Scoring table:

IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 118133 segs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

1: gb\_ba1:\*  
2: gb\_ba2:\*  
3: gb\_om:\*  
4: gb\_ov:\*  
5: gb\_ph:\*  
6: gb\_pl1:\*  
7: gb\_pl2:\*  
8: gb\_pl3:\*  
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28: em\_v1:\*  
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80: gb\_v12:\*  
81: gb\_pat1:\*  
82: gb\_pat2:\*  
83: em\_htg0:\*  
84: gb\_htg24:\*  
85: gb\_pr8:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	719.4	98.7	729	12	AC0131532
2	717.8	98.5	768	81	A57272
3	716.2	98.2	749	81	A59386
4	716.2	98.2	1611	81	A59381
5	565.2	77.5	912	12	AB030249
6	550.8	75.5	864	12	XX031739
7	500.4	68.5	747	11	MMVHVKEG
8	476.2	65.3	732	12	XX044796
9	460.8	63.2	747	12	AC0131533
10	455.4	62.5	738	12	AF064776
11	452.2	62.3	1314	81	A68604
12	446.4	61.2	759	12	SC0250763
13	432.2	59.3	753	11	AX003776
14	432.2	59.3	810	81	A45006
15	432.2	59.3	1637	12	AX006750
16	429	58.9	753	11	AX003768
17	426.4	58.5	786	11	MMU31195
18	425.2	58.3	1679	81	AR054409
19	425	58.3	747	12	AF226875
20	420.2	57.5	729	12	AF162709
21	418.4	57.4	723	12	AF169027

22	415.2	57.0	843	81	A83223	A83223 Sequence 43
23	415.2	57.0	1998	81	A83230	A83230 Sequence 50
24	386.2	53.0	795	11	MMSCFVP25	270662 Artificial
25	385.2	52.8	804	81	A95255	A95255 Sequence 1
26	380	52.1	4354	12	ASY14583	V14583 Artificial
27	377.4	51.8	726	11	MMU20617	U20617 Mus musculus
28	377.4	51.8	864	81	A83227	A83227 Sequence 47
29	377.4	51.8	2019	81	A83211	A83211 Sequence 31
30	377.4	51.8	2025	81	A83217	A83217 Sequence 37
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32	367.8	50.5	729	11	AF002242	AF002242 Mus muscu
33	364.2	50.0	810	11	MMU62527	U62527 Mus musculus
34	364	49.9	723	12	SC0250761	AJ250761 Mus muscu
35	361.8	49.6	722	12	S57990	S57990 B3(FV)-PE40
36	361.8	49.6	772	81	AR085460	AR085460 Sequence
37	361.8	49.6	772	81	AR088866	AR088866 Sequence
38	361.8	49.6	772	81	I36723	I36723 Sequence 33
39	360.8	49.5	744	11	AX003782	AX003782 Sequence
40	358	49.1	747	81	A33046	A33046 Anti-oxazol
41	357.6	49.1	744	11	AX003772	AX003772 Sequence
42	357	49.0	798	11	AF000955	AF000955 Mus muscu
43	356.8	48.9	1725	13	AX001509	AX001509 Sequence
44	356.2	48.9	738	11	AF141321	AF141321 Mus muscu
45	355.6	48.8	738	11	MMU40581	U40581 Mus musculus

## ALIGNMENTS

RESULT 1  
AC013532 729 bp mRNA SYN 16-MAR-2000  
AC013532  
DEFINITION Synthetic construct for anti-p53 scFv antibody (sefv421) containing linker sequence.

ACCESSION AJ131532.1 GI:4033863  
KEYWORDS antibody; immunoglobulin superfamily; scFv; variable region.  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 729)  
AUTHORS Caron de Fromental, C., Gruel, N., Venot, C., Debussche, L.,  
Conseiller, E., Drenth, C., Teillac, J. L., Tocque, B. and Bracco, L.  
TITLE Restoration of transcriptional activity of p53 mutants in human  
tumour cells by intracellular expression of anti-p53 single chain  
Fv fragments  
JOURNAL Oncogene 18 (2), 551-557 (1999)  
MEDLINE 99124402  
REFERENCE 2 (bases 1 to 729)  
AUTHORS de Fromental, C.  
TITLE Direct Submission  
JOURNAL Submitted (16-DEC-1998) de Fromental C., U 380 INSERM, Institut  
Cochin de Genetique Moleculaire, 22 rue Mechain PARIS, 75014,  
FRANCE

## FEATURES

## CDS

1. 729  
Location/Qualifiers  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/cell\_line="Pab421"  
/cell\_type="hybridoma"  
/focus  
/note="synthetic"  
/codon\_start=1  
/transl\_table=1  
/product="anti-p53 scFv antibody (scfv421)"  
/protein\_id="CA10385.1"  
/db\_xref="GI:4033864"  
/translation="OVLQOQSGAEIVRSGLSKTSAGFNKIDYWMHWKORPEOG  
LEWIGMDPENDEYAKRFGKATMDTSNMYAQLDLSASDPTAVYCNFYGDA  
LDYNGCCTTVYVSSGGGSGGSDVIMQPTLTSLVTIGQPSISCKSSQSL  
LDSGKTYLAWLORPGSPKRLIYVSKLDSGVDRRTGSGSDIFLKNRVAED  
LGVIYCWGTHSPITFGAGTKLEIK"

source	1. 729	/organism="Mus musculus"	/db_xref="taxon:10090"
V_region	1. 116	/product="immunoglobulin heavy chain variable region"	
source	1. 116	/organism="Mus musculus"	/db_xref="taxon:10090"
misc_feature	117. 131	/note="linker sequence"	
V_region	132. 243	/product="immunoglobulin light chain variable region"	
source	132. 243	/organism="Mus musculus"	/db_xref="taxon:10090"
BASE COUNT	176 a, 168 c, 205 g, 180 t		
ORIGIN			
Query Match	98.7%; Score 719.4; DB 12; Length 729;		
Best Local Similarity	99.2%; Pred. No. 1.3e-212;		
Matches	723; Conservative 0; Mismatches 6; Indels 0; Gaps 0;		
QY	1	caggtgcagctgcagcagctgcgggcaagctgtgaggtcagggtcagtcagtgtg	60
DB	1	CAGGTGACGCTGCACAGCTGTGGGCGACAGCTGTGAGGTCTGAGGTCTGAGGTG	60
QY	61	tcctgcagcagcttcgtgcttcacattaaagactatcatgctggtggtgaagcagg	120
DB	61	TCTGCAACGCTTCTGGCTTCACTTAAGACTTATGACCTGAGGTGAGGTGAGGTG	120
QY	121	cctgacagcagcctgagtgagtgatgagtgatgagtgatgagtgatgagtgatgag	180
DB	121	CCTGAACAGCGCGCTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTG	180
QY	181	gccccgaagttcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag	240
DB	181	GCCCCGAAGTTCAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGG	240
QY	241	ctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag	300
DB	241	CTGCAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	300
QY	301	gatgcttgagctatggggcagcagcagcagcagcagcagcagcagcagcagcagcag	360
DB	301	GATGCTTGAGCTATTTGGGGCCAGGACAGGACAGGACAGGACAGGACAGGACAGG	360
QY	361	tcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag	420
DB	361	TCAGCGGAGGAGGCTGCGGCGTGGCGATCGATGATGATGATGATGATGATGATGATG	420
QY	421	acttgctgagtgatgagcagcagcagcagcagcagcagcagcagcagcagcagcag	480
DB	421	ACTTGTGGTTCATTGATGAGACACAGCCTTCATCTTTCGAACTCAAGTCAGGCTTC	480
QY	481	ttgagtaagtgatgagaaagacatattgagtgatgagtgatgagtgatgagtgatgag	540
DB	481	TTGATATGATGAGAAACATATTGATGATGATGATGATGATGATGATGATGATGATG	540
QY	541	aagcgcctaatctatctggtgtctaactgagcagcagcagcagcagcagcagcagcag	600
DB	541	AAGCGCTTAATCTATCTGTGTCTTAATGAGCTCTGAGGCTCTGAGGCTCTGAGG	600
QY	601	agtgatcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag	660
DB	601	AGTGATCAGGAGCAGGCTTCACTTAATTAATTAATTAATTAATTAATTAATTAATTA	660
QY	661	gttatatttcovggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag	720
DB	661	GTTTATTTCCTGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG	720
QY	721	gaatcaaa 729	

Db 721 GAATTA 729

RESULT 2  
LOCUS A57272 768 bp DNA PAT 03-MAR-1998  
DEFINITION Sequence 4 from Patent MO9630512.  
ACCESSION A57272  
VERSION A57272.1 GI:3713167  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 768)  
AUTHORS Bracco, L., Schweighoffer, F. and Tocque, B.  
TITLE CONDITIONAL EXPRESSION SYSTEM  
JOURNAL Patent: WO 9630512-A 4 03-OCT-1996;  
COMMENT RHONE-POULENC RORER SA (FR)  
Other publication AU 5402096 961016  
Other publication FR 2732348 961004.  
FEATURES  
Location/Qualifiers  
source 1..768  
/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 181 a 185 c 218 g 184 t

Query Match 98.5%; Score 717.8; DB 81; Length 768;  
Best Local Similarity 99.0%; Pred. No. 4.2e-212;  
Matches 722; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 caggtgacgtcgcagcgcgtcgtgagcagcgtgtgtgagcagggcctcaagtcagt 60  
DB 28 CAGGTGACGTGCGACGCTGCGGCGACGCTGTGTAAGCGGCGCTCAGTCAAGTTG 87

QY 61 tccgcacagcttcgtgcttaacattaaagactactatgacagtggtgaagcagag 120  
DB 88 TCCGCGACAGCTTCTGCTTCAACATTAAAGACTACTATATGCACTGGTGAAGCAAGG 147

QY 121 cctgaacagggccttgaggtgattgtgattgacctgaagaagtgtgactgaatat 180  
DB 148 CCTGAACAGGGCCTGAGTGGATGTGATGATCTTAAGATGGTGAATGATAT 207

QY 181 gccccgaagttccagggcagggccactatgacatgcacacatctccataacagcctac 240  
DB 208 GCCCGAAGTTCAGGGCAGGCGCACATGACATGACACATCTCCATATACGCTAC 267

QY 241 ctgacagtcagcagcctgcgcatctgagagacatgcgctctattatgttaatttaagcg 300  
DB 268 CTGACAGTCAGCAGCCTGCGCATCTGAAGACATGCGCTGTATTTATTTTACGGG 327

QY 301 gatgcttgactatgtgggccaagggacagcaggttcacgctctcctcaggttgagggcgt 360  
DB 328 GATGCTTTGGACATGTGGGCGCAAGGACACGCTGTCACCGCTCTCCTAGGGGAGG 387

QY 361 tcagggcagaggtggtcctgcggtgctgcgagtcggaatgtttgatgacccaactcaatc 420  
DB 388 TCAAGCGGAGGTGCTCTGCGGGTGGGCGGATCGGATCTTTGATGAGCCCAACCTCCATC 447

QY 421 acttgccggttaccattggaacacagcagcctccatctcttggaagttcaagtcagagctc 480  
DB 448 ACTTTGCGGTTACCATTTGGACACAGCTCCATCTCTTGCAAGTCAAGTCAGGCTC 507

QY 481 ttgatatgtatggaagacatatltgaattggtgttaagagggccagggccagtcctca 540  
DB 508 TTGATATGTATGGAATAACATATTGCAATTGTTGTACAGAGGCGCAGGCACTCCCA 567

QY 541 aagggcctaatactatctcgtggtctaaactgagcctgagtcctgcagagttcaactggc 600  
DB 568 AAGGCGCTAATCTATCTGGGTGTCTAAAGCTGACCTGAGAGCCCTGACAGGTTCACTGGC 627

QY 601 agtgcacagggacagatttcaacactgaatacaacagagtgagggagtgagatttgga 660

Db 628 AGTGATCAGGGACAGATTTCACACTTAATACACAGAGTGGAGCTGAGATTTGGGA 687

QY 661 gttattatctgcgaaggttacacattctcgcctcaggttcggtgctggcaccagctg 720  
DB 688 GTTATTATATGCTGGCAAGGTACACATCTCCGCTTACGTTCCGCTGCTGGCACCAGCTG 747

QY 721 gaaatcaaa 729  
DB 748 GAATTTAA 756

RESULT 3  
LOCUS A59386 749 bp DNA PAT 06-MAR-1998  
DEFINITION Sequence 36 from Patent WO9704092.  
ACCESSION A59386  
VERSION A59386.1 GI:3714722  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 749)  
AUTHORS Counselier, E. and Bracco, L.  
TITLE P53 PROTEIN VARIANTS AND THERAPEUTICAL USES THEREOF  
JOURNAL Patent: WO 9704092-A 36 06-FEB-1997;  
COMMENT RHONE-POULENC RORER SA (FR)  
Other publication FR 2736915 970124.  
FEATURES  
Location/Qualifiers  
source 1..749  
/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 173 a 179 c 221 g 176 t

Query Match 98.2%; Score 716.2; DB 81; Length 749;  
Best Local Similarity 98.9%; Pred. No. 1.3e-211;  
Matches 721; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 caggtcagcttgacagcagctcgtgagcagcgtgtgtgagtcagggcctcagtcagt 60  
DB 10 CAGGTGACGTGCGACGAGTGCAGGCGCAGAGCTGTGGGCGCAGGCGCTCAGTCAAGTTG 69

QY 61 tccgtcacagcttcgtgcttaacattaaagactactatgacatggtgagagcagag 120  
DB 70 TCCGTGACAGCTTCTGCTTCAACATTAAAGACTACTATATGCACTGGGTAAGCAGAGG 129

QY 121 cctgaacagggccttgaggtgattgtgattgacctgagagaatgtgtactgaatat 180  
DB 130 CCTGAACAGGSCCTGAGTGGATGTGATGATCTGAGATGGTGAATGATGATAT 189

QY 181 gccccgaagttccagggcagggccactatgacatgcacacacatccccaataacagcctac 240  
DB 190 GCCCGAAGTTCAGGGCAGGCGCACATGACATGACAGACACATCTCCATATACGCTAC 249

QY 241 ctgacagtcagcagcctgcgcatctgagagacatgcgctctatattgttaatttaagcg 300  
DB 250 CTGACAGTCAGCAGCCTGCGCATCTGAAGACATGCGCTGTATTTATTTTACGGG 309

QY 301 gatgcttgactatgtgggccaagggacagcaggttcacgctctcctcaggttgagggcgt 360  
DB 310 GATGCTTTGGACATGTGGGCGCAAGGACACGCTGTCCTCCTCAGTGAAGGCGGT 369

QY 361 tcagggcagaggtggtcctgcggtgctgcgagtcggaatgtttgatgacccaactccactc 420  
DB 370 TCAAGGGGAGGCTGCTCTGCGGGTGGGCGGATCGGATGCTTTGATGACCAACTCCACTC 429

QY 421 acttgccggttaccattggaacacagcagcctccatctcttggaagttcaagtcagagctc 480  
DB 430 ACTTTGCGGTTACCATTTGGACACAGCTCCATCTCTTGCAAGTCAAGTCAAGAGCTC 485

QY 481 ttgatatgtatggaagacatatltgaattggtgttcaagagggccagggccagtcctca 540

	Query Match	Best Local Similarity	98.28	Score 716.2	DB 81	Length 1611
	Matches	721	Conservative	0	Mismatches	8
					Indels	0
					Gaps	
Qy	1	caggtgcacgtcgcacagctctgtggcgacagctctgtgaagtcacggggccctcagtcgaattg	60			
Dy	7	CAGGTGCAGCTGCACGAGGATCAGGGCGCAGAGCTTGTGGCGATCAGGGCCCTACGCAAGTTG	66			
Qy	61	tccttcacaaagctttgtgcttaacattaaagaacacactatgcacctgtgtggaagcagaag	120			
Dy	67	TCCTGCACAGCTTCTGGCTTAAACATTAAAGACTACTATATGCCACTGGGGAAGCCAGAGG	126			
Qy	121	cctgaacagggccctgtgaattgtgaattgtgaattgtatcctcgaagaattgtgaactgaatat	180			

AB030249	5	RESULT
AB030249	912 bp	DNA
LOCUS		SYN
DEFINITION	Synthetic Mus musculus gene for 3C10 single chain antibody,	22-OCT-1999
ACCESSION	AB030249	
VERSION	AB030249.1	GI:5596361
KEYWORDS	light chain variable domain; heavy chain variable domain; 3C10 single chain antibody.	
SOURCE	synthetic construct DNA.	
ORGANISM	synthetic construct	
REFERENCE	artificial sequence.	
AUTHORS	1 (sites)	
	Okamoto,S., Yoshikawa,K., Obata,Y., Shibuya,M., Aoki,S., Yoshida,J.	
	and Takahashi,T.	
TITLE	Monoclonal antibody against the fusion junction of a	
	deletion-mutant epidermal growth factor receptor	
JOURNAL	Br. J. Cancer 73 (11), 1366-1372 (1996)	
MEDLINE	96249052	
REFERENCE	2 (sites).	
AUTHORS	Nakayashiki,N., Yoshikawa,K., Nakamura,K., Hanai,N., Okamoto,S.,	
	Mitump,M., Wakabayashi,T., Saga,S., Yoshida,J. and Takahashi,T.	
TITLE	Production of a single chain variable fragment antibody recognizing	
JOURNAL	type III mutant epidermal growth factor receptor	
REFERENCE	unpublished (1999)	
AUTHORS	3 (bases 1 to 912)	
TITLE	Yoshikawa,K. and Nakayashiki,N.	
JOURNAL	Direct Submission	
	Submitted (21-JUL-1999) to the DDBJ/EMBL/Genbank databases.	
	Kazuhito Yoshikawa, Aichi Medical University, Department of	

Pathology: Yatako, Karimata 21, Nagakute, Aichi 480-1195, Japan  
(E-mail: yoshikawamugw.aichi.med-u.ac.jp,  
Tel: 81-561-62-3311 (ex. 2265); Fax: 81-561-62-9318)

## FEATURES

source

Location/Qualifiers

1. 912

/organism="synthetic construct"

/db\_xref="taxon:32630"

/note="cloned from mouse hybridoma producing 3C10  
monoclonal antibody recognizing a type III mutant BGF  
receptor"

gene

1. 912

/gene="3C10 scFv"

CDS

1. 912

/gene="3C10 scFv"

/note="contains single chain Fv"

/codon\_start=1

/transl\_table=11

/product="3C10 single chain antibody"

/protein\_id="BA82610.1"

/db\_xref="GI:5596362"

/translation="MEIQOSGAELVKGASVKSCTGPGNIEHYTHMYKQTEQ  
GLEWIRIDPENDETKYPFOGRATITADTSSNYVLDLSITSEDAIVYICARLG  
VWPGETITLVSSGGSGSGSGGSHMDVMTQSPPLTSLVAIGQASISCKSSQ  
LIDSDKTYLMLQRPQSPKRLISLVSKLSDGVPDRFTGSGGDFTLRISRYEAE  
DLGIYCMQGTGHPGFPGSGTKLEIKRSGGSGGSGGSGIMRSHHHHGMASMTGQ  
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1. 345

/gene="3C10 scFv"

/note="encodes heavy chain variable domain"

misc-feature

346..390

/gene="3C10 scFv"

/note="encodes linker sequence"

misc-feature

391..783

/gene="3C10 scFv"

/note="encodes light chain variable domain"

BASE COUNT

225 a 209 c 264 g 214 t

ORIGIN

Query Match

Best Local Similarity 87.7%; Score 565.2; DB 12; Length 912;

Matches 644; Conservative 0; Mismatches 78; Indels 12; Gaps 2;

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QY 2 aggtgagcgtgagcagctggtgagcagcgttgtgagtcaggggagcctcgaagtgt 61
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Db 5 AGATCCAGCTGCGACATCTGGGCGACAACTTGGAAGCCAGGCGCTCAGTCAAGCTG 64
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QY 62 ccgtgacagcttctggtcaacattaaactactatgacatggtgtgaagcagagc 121
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Db 65 CCGACAGAGTCTGCTGCTTACATTGAACATGACTATATCTGCTGCTGACAGAGGA 124
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QY 122 ctgaacagggcctgtgagtgatgtgacgttaccctggaatgtgtactgaatg 181
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QY 182 ccccgaggtccagggaagcgaactatgactcgaacacatctcgaacagccacc 241
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Db 185 GCCCAATATTCAGGAGGAGGCCACTTAACAGACAGACATCTCCACACAGCTACAC 244
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Db 245 TGCACACACAGCAGCTCAATCTGAGACACTGCGCTTATCTGCGCCTTCGCGG-- 302
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QY 362 caggcgaggttgagctctggcggtgagc-----gagtggtttatbaccacaactc 415
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Db 359 CCGGTGGTGGTGGTCCGGAGAGTGGTTCACATATGATGATGATGATGATGATGATG 418
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QY 416 cactcaattgtcggtacattggaacacagcctccatctcttgaagtcaagtaca 475
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Db 419 CACTCAGCTATACGGTGGCCATTGGAACATTCAGCTTCATCTCTTGCAGTCAAGTACAGA 478
QY 476 ggcctctgtagtattgtaaaagacatattgaattggtttacagagccagccact 535
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Db 479 GCCTCTAATATGATGAGGAAGACATATTGGAATGGTGTGTACAGAGGCCAGGCACT 538
QY 536 ctccaagagcccaactctctggtctcaaacctgagccttgagtcctcagagttca 595
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Db 539 CTCACAAAGCGCCATACCTCTGTGTCTTAACCTGACCTGTGAGTCCCTGACAGGTTCA 598
QY 596 ctggcagtgatcagagagacattcacactgaataacacagagtgagtgagtgat 655
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Db 599 CTCGAGTGTGATCAGGAGACAGATTTCACACTGAGATCAGAGATGAGAGGCTGAGAGATT 658
QY 656 tggagttattattattctgagcaaggtacacattctcctcagcttgcgtgagacca 715
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Db 659 TGGGAATTTATTTATTTCTGCAAGGTACACATTTCTCTGGAGCTGGGTGAGGAGCA 718
QY 716 agctggaatcaaa 729
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Db 719 AGCTGAGATMAAA 732
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RESULT 6
LOCUS XXU31739 864 bp DNA SYN 05-SEP-1995
DEFINITION Single chain antibody SCA 13.1 gene, complete cds.
ACCESSION U31739
VERSION U31739.1 GI:975304
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 864)
AUTHORS Nardone,F., Spano,F. and Crisanti,A.
TITLE Direct Submission
JOURNAL Submitted (17-JUL-1995) Francesco Nardone, Istituto di
parasitologia, University of Rome 'La Sapienza', Piazzale Aldo
Moro 5, Roma, RM 00185, Italy
FEATURES
source Location/Qualifiers
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CDS 1..864
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MTQPLSPISIGDQASISCRSSQSVISNNGTITLWLRQSGPKLILRVSRFS
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LISEEDLNGAA"
67..426
/note="variable region from heavy chain"
misc-feature 157..161
/note="encodes CDR 1"
misc-feature 214..264
/note="encodes CDR 2"
misc-feature 361..393
/note="encodes CDR 3"
misc-feature 427..471
/note="encodes linker peptide"
misc-feature 472..810
/note="variable region from light chain"
misc-feature 541..588
/note="encodes CDR 1"

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Query Match	75.6%	Score 550.8	DB 12	Length 864
Best Local Similarity	85.3%	Pred. No. 3.7e-160		
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misc_feature	/note="encodes CDR 2"			
misc_feature	751..774			
misc_feature	/note="encodes CDR 3"			
misc_feature	811..864			
BASE COUNT	205 a	222 c	234 g	203 t
ORIGIN				
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Best Local Similarity	85.3% <td>Pred. No. 3.7e-160</td> <td></td> <td></td>	Pred. No. 3.7e-160		
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				Gaps 1
misc_feature	/note="encodes CDR 2"			
misc_feature	751..774			
misc_feature	/note="encodes CDR 3"			
misc_feature	811..864			
BASE COUNT	205 a	222 c	234 g	203 t
ORIGIN				

[illegible]















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OM nucleic - nucleic search, using sw model

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Run on:      February 17, 2001, 22:08:36      Search time 936.51 Seconds
              (without alignments)
              5454.783 Million cell updates/sec
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Perfect score:  729
Sequence:       1  caggtgcagctgcagcagtc.....gcaccaagctggaatcaaa 729

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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44:	em.esthunn1.*
45:	em.esthunn2.*
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74:	em.esthunn31.*
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111:	em.esthunn68.*
112:	em.esthunn69.*
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114:	em.esthunn71.*
115:	em.esthunn72.*
116:	em.esthunn73.*

117: em\_estp16:\*  
 118: em\_estp17:\*  
 119: em\_estp18:\*  
 120: em\_estp19:\*  
 121: em\_estp20:\*  
 122: em\_estp21:\*  
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 183: em\_estp82:\*  
 184: em\_estp83:\*  
 185: em\_estp84:\*  
 186: em\_estp85:\*  
 187: em\_estp86:\*  
 188: em\_estp87:\*  
 189: em\_estp88:\*

190: gb\_gss25:\*  
 191: gb\_gss26:\*  
 192: gb\_gss27:\*  
 193: gb\_gss28:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	279.4	38.3	1057	106	BE306420
2	235.2	32.3	793	106	BE307894
3	232.8	31.9	471	90	AM405772
4	232.8	31.9	614	90	AM405187
5	229.2	31.4	454	90	AM406883
6	227.2	31.2	444	90	AM406448
7	223.4	30.6	363	7	AA464313
8	223.4	30.6	425	24	AT734035
9	223.4	30.6	442	7	AA405415
10	221.8	30.4	488	90	AM405725
11	219.2	30.1	468	136	BE829853
12	218.2	29.9	456	90	AM404683
13	218.2	29.9	488	141	H25625
14	214.8	29.5	911	106	BE286958
15	213.4	29.3	353	90	AM406473
16	210.6	28.9	400	96	AM912881
17	210.4	28.9	358	136	BE850886
18	209.2	28.7	653	90	AM404795
19	206.6	28.3	739	106	BE284158
20	204.8	28.1	379	96	AM908776
21	204.4	28.0	512	139	BE023434
22	199.8	27.4	772	106	BE285427
23	198.4	27.2	406	139	BE016722
24	198.4	27.2	491	93	AM632401
25	197.2	27.0	316	90	AM405157
26	194.6	26.7	484	90	AM404368
27	193.8	26.6	507	139	BE015548
28	193.4	26.5	409	111	BE719012
29	193.2	26.5	467	141	H27034
30	193.2	26.5	543	90	AM404804
31	192.4	26.4	473	106	BE307170
32	192.4	26.4	567	106	BE287568
33	192.2	26.4	485	95	AM806366
34	192.2	26.3	420	90	AM406361
35	192.2	26.3	486	95	AM806391
36	191.2	26.2	459	95	AM806364
37	191.2	26.2	374	9	AA602059
38	190.6	26.2	596	106	BE310080
39	190.6	26.1	601	172	AZ447391
40	189.8	26.0	554	174	AZ505978
41	189.6	26.0	534	93	AM658126
42	188.2	25.8	456	104	BE144269
43	187.2	25.7	544	93	AM655441
44	186.8	25.6	287	8	AA496610
45	184	25.2	439	104	BE136816

## ALIGNMENTS

RESULT 1  
 BE306420 \* 1057 bp mRNA  
 LOCUS 601103347p1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:3495755 5',  
 DEFINITION  
 mRNA sequence.  
 ACCESSION BE306420  
 VERSION BE306420.1 GI:9159604  
 KEYWORDS EST.  
 SOURCE house mouse.



ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 1057)  
AUTHORS NIH-MGC  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLM8534 row: n column: 12  
High quality sequence stop: 695.  
Location/Qualifiers  
1..1057  
/organism="Mus musculus"  
/strain="C57BL/6J (f6al)"  
/db\_xref="taxon:10090"  
/clone="IMAGE:349575"  
/clone\_lib="NCI\_CGAP\_Lu29"  
/tissue\_type="spontaneous tumor, metastatic to mammary."  
/dev\_stage="7 months"  
/lab\_host="DH10B"  
/note="Organ: Lung; Vector: PCMV-SPORE6; Site: 1; SalI; Site: 2; NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 274 a 289 c 273 g 221 t  
ORIGIN

Query Match 38.3%; Score 279.4; DB 106; Length 1057;  
Best Local Similarity 88.8%; Pred. No. 2.3e-73;  
Matches 317; Conservative 0; Mismatches 31; Indels 9; Gaps 1;

QY 2 aggtcagctgcagcagctctggcagagcttgatgagtcaggagcctcaagtcagt 61  
|||||  
DB 78 AGGTTGAGCTGACAGAGCTGCGGAGAGCTGTGAGGCCAGGGGCTCAGTCAAGTTG 137  
|||||  
QY 62 ccgcagcagcttgcgttaacataaagacacacacacacacacacacacacacac 121  
|||||  
DB 138 CCGGACAGCTTGTGCTTCAACATTAAAGACAGCCTTATGACATGGGTAAAGCAGAGGC 197  
|||||  
QY 122 ctgaacagagcctggagtgatgagtcgagtcgagtcgagtcgagtcgagtcgagtcg 181  
|||||  
DB 198 CTGAACAGGCGCTGGAGTGGATGGATGGATGGATGGATGGATGGATGGATGGATGG 257  
|||||  
QY 182 ccccgagagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 241  
|||||  
DB 258 CCGGAGAGTCCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGG 317  
|||||  
QY 242 tgaagctcagcagcctggagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtc 292  
|||||  
DB 318 TGCAGCTCAGCAGCCTGACATCTGAGAGACACTCCATCTATTACTGTGCTAGAAACCTTT 377  
|||||  
QY 293 ttcaagggagtcgcttgagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 349  
|||||  
DB 378 TGTATGTTGTTACTAGACTACTGGGGCCAAAGCAGCACTATACAGATGCTCTCAG 434  
|||||

RESULT 2  
LOCUS BE307894 793 bp mRNA EST 13-JUL-2000  
DEFINITION 601096548f1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:3491195 5',  
ACCESSION BE307894  
VERSION BE307894.1 GI:9163704

KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 793)  
AUTHORS NIH-MGC  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLM8534 row: p column: 12  
High quality sequence stop: 514.  
Location/Qualifiers  
1..793  
/organism="Mus musculus"  
/strain="C57/B6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3491195"  
/clone\_lib="NCI\_CGAP\_Mam5"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: PCMV-SPORE6; Site: 1; SalI; Site: 2; NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

BASE COUNT 156 a 210 c 217 g 210 t  
ORIGIN

Query Match 32.3%; Score 235.2; DB 106; Length 793;  
Best Local Similarity 81.2%; Pred. No. 4.7e-60;  
Matches 273; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 364 gatgtttgatgacccaactccactcacttctgtgtggttaccattggaaaccacctcc 453  
|||||  
DB 82 GAGTGTGATGACCCAACTCCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 141  
|||||  
QY 454 atctctcgaagtcagagtcagagtcagagtcagagtcagagtcagagtcagagtcagagtc 513  
|||||  
DB 142 ACTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 201  
|||||  
QY 514 ttgttacagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 573  
|||||  
DB 202 TTCTGCGCAAGCAGGCGGAGCTCCAAAGCTCTGATCAACAGAGTTTCCAAAGCATTT 261  
|||||  
QY 574 tctgagtcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 633  
|||||  
DB 262 TCTGGGCTCCAGACAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 321  
|||||  
QY 634 aacagagtcagagtcagagtcagagtcagagtcagagtcagagtcagagtcagagtcagagtc 693  
|||||  
DB 322 ACCAGAGTGAGGCTGAGGATCTGGAGATTTTCTGCTCAAGTACATGATGTCG 381  
|||||  
QY 694 ctcaagctcgtgtgctggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 729  
|||||  
DB 382 CTCACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 417  
|||||

RESULT 3  
LOCUS AM405772 471 bp mRNA EST 16-FEB-2000  
DEFINITION UI-HF-BLJ-abp-c-06-0-UI.1 NIH\_MGC\_37 Homo sapiens cDNA clone

IMAGE:3057394.5', mRNA sequence.  
ACCESSION AM405172  
VERSION AM405172.1 GI:6924829  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 471)  
NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: M.B. Soares Lab  
CDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/dbip/image/image.html](http://www.bio.llnl.gov/dbip/image/image.html)  
Seq primer: M13 Forward  
Location/Qualifiers  
1. 471  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3057394"  
/clone\_1ib="NIH-MGC\_37"  
/tissue\_type="lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (LT1)"  
/note="Vector: pTZ19-Pac; Site\_1: NotI; Site\_2: Eco RI;  
constructed from size fractionated cytoplasmic mRNA  
(1.5-2.5kb). Directionally cloned. Cells provided by Louis  
M. Staudt, Ph.D. Library preparation by Maria de Fatima  
Bonaldi, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 107 a 124 c 119 g 121 t  
ORIGIN

Query Match 31.9%; Score 232.8; DB 90; Length 471;  
Best Local Similarity 79.3%; Pred. No. 2.1e-59;  
Matches 276; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 382 ggtggcgatcgatgttttgatgacccaactccactcttgcgtttaccattga 441  
DB 15 GGATCCAGTCAGATATGTGATGACCCAGACACCTCTCTGCGCACCCCTGA 74  
QY 442 caacgagctcattctcttcgaagtcagagcctcttgatagatgagaaagaa 501  
DB 75 CAGTCGGCTCCATCTCTGCAAGTCAAGCTCCTCTCTGCGCACCCCTGA 134  
QY 502 tattgaattggtgttgaagagcagcagcttccaaagcgcctaatctatctg 561  
DB 135 TATTGTATTGATGACCTGCAAGCAAGCCAGCTCCTGATCTATGAAGTT 194  
QY 562 tctaaacttgacctgagatcccttgacaggttcaactgagcagtgagagagattc 621  
DB 195 TCCAAACGGTCTCTGAGAGCCAGATAGGTTAGTGCGACGGGTCAGAGCAAGATTTC 254  
QY 622 acactgaataaacaagagtgagagctgagagatttggaatttatattatgctgcaag 681  
DB 255 ACACCTAATAATCACCAGGAGGAGGCTGAGAGATGTTGGGGTTTATTCATGCAAAAGT 314  
QY 682 acacattctccgctcaagctggtgtgctgaccaaagctggaatacaaa 729  
DB 315 ATACAGCTTCCTCTCACTTCCGCGAGGAGCAAGGTGAGATCAAA 362  
RESULT 4

AM405187 614 bp mRNA EST 16-FEB-2000  
LOCUS UI-HF-BL0-acb-c-06-0-UI.r1 NIH-MGC\_37 Homo sapiens CDNA clone  
DEFINITION IMAGE:3058546.5', mRNA sequence.  
ACCESSION AM405187  
VERSION AM405187.1 GI:6924244  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 614)  
NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: M.B. Soares Lab  
CDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/dbip/image/image.html](http://www.bio.llnl.gov/dbip/image/image.html)  
Seq primer: M13 Forward  
Location/Qualifiers  
1. 614  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3058546"  
/clone\_1ib="NIH-MGC\_37"  
/tissue\_type="lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (LT1)"  
/note="Vector: pTZ19-Pac; Site\_1: NotI; Site\_2: Eco RI;  
constructed from size fractionated cytoplasmic mRNA  
(1.5-2.5kb). Directionally cloned. Cells provided by Louis  
M. Staudt, Ph.D. Library preparation by Maria de Fatima  
Bonaldi, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 146 e 169 c 160 g 139 t  
ORIGIN

Query Match 31.9%; Score 232.8; DB 90; Length 614;  
Best Local Similarity 79.3%; Pred. No. 2.3e-59;  
Matches 276; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 382 ggtggcgatcgatgttttgatgacccaactccactcttgcgtttaccattga 441  
DB 55 GGATCCAGTCAGATATGTGATGACCCAGACACCTCTCTGCGCACCCCTGA 114  
QY 442 caacgagctcattctcttcgaagtcagagcctcttgatagatgagaaagaa 501  
DB 115 CAGCGCGCTCCATCTCTGCAAGTCAAGCTCCTCTCTGCGCACCCCTGA 174  
QY 502 tattgaattggtgttgaagagcagcagcttccaaagcgcctaatctatctg 561  
DB 175 TATTGTATTGATGACCTGCAAGCAAGCCAGCTCCTGATCTATGAAGTT 234  
QY 562 tctaaacttgacctgagatcccttgacaggttcaactgagcagtgagagagattc 621  
DB 235 TCCAAACGGTCTCTGAGAGCCAGATAGGTTAGTGCGACGGGTCAGAGCAAGATTTC 294  
QY 622 acactgaataaacaagagtgagagctgagagatttggaatttatattatgctgcaag 681  
DB 295 ACACCTGCAAAACACTGCTGAGAGGCTGAGAGATGTTGGGGTTTATTCATGCAAAAGT 354  
QY 682 acacattctccgctcaagctggtgtgctgaccaaagctggaatacaaa 729  
DB 355 ATACAGCTTCCTCTCACTTCCGCGAGGAGCAAGGTGAGATCAAA 402  
RESULT 4

FEATURES	Source
LOCUS	AM406883
DEFINITION	AM406883 454 bp mRNA EST 16-FEB-2000
ACCESSION	U1-HF-BLO-adg-h-03-0-UI.1 NIH_MGC_37 Homo sapiens CDNA clone
VERSION	IMAGE:3061493 5', mRNA sequence.
KEYWORDS	AM406883
ORGANISM	AM406883.1 GI:6925940
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL	1 (bases 1 to 454)
COMMENT	NIH-MGC <a href="http://www.ncbi.nlm.nih.gov/MGC/">http://www.ncbi.nlm.nih.gov/MGC/</a> .
	National Institutes of Health, Mammalian Gene Collection (MGC)
	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.
	Tel: (301) 496-1550
	Email: Robert.Strausberg@nih.gov
	Eco RI site shown at the beginning of the sequence.
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
	CDNA Library Preparation: Louis M. Staudt, M.D., Ph.D.
	CDNA Library Arrayed by: M.B. Soares Lab
	CDNA Sequencing by: M.B. Soares Lab
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LINL at:
	<a href="http://www-bio.lnl.gov/bdrrp/image/image.html">www-bio.lnl.gov/bdrrp/image/image.html</a>
	Seq primer: M13 Forward
	Location/Qualifiers
	1..454

[illegible]

RESULT	6	
LOCUS	AM406448	
DEFINITION	AM406448 444 bp mRNA	EST
ACCESSION	U1-HF-B10.acr-c-05-0-U1.r1 NIH_MGC_37	16-FEB-2000
VERSION	IMAGE:3060080.5	Homo sapiens CDNA clone
KEYWORDS	AM406448.1	GI:6925505
SOURCE	EST	
ORGANISM	human	
REFERENCE	Homo sapiens	
AUTHORS	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
JOURNAL	NIH-MGC <a href="http://www.ncbi.nlm.nih.gov/MGC/">http://www.ncbi.nlm.nih.gov/MGC/</a>	
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)	
	Unpublished (1999)	
	Contact: Robert Strausberg, Ph.D.	
	Tel: (301) 496-1550	
	Email: <a href="mailto:Robert.Strausberg@nih.gov">Robert.Strausberg@nih.gov</a>	
	Eco RI site shown at the beginning of the sequence.	
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.	
	CDNA Library Preparation: M.B. Soares Lab	
	CDNA Library Arrayed by: M.B. Soares Lab	
	DNA Sequencing by: M.B. Soares Lab	
	Clone distribution: MGC clone distribution information can be	
	found through the I.M.A.G.E. Consortium/BLNLT at:	
	<a href="http://www-bio.lnl.gov/brdp/image/image.html">www-bio.lnl.gov/brdp/image/image.html</a>	
	Seq primer: M13 Forward.	

FEATURES		Location/Qualifiers
SOURCE		1..444
		/organism="Homo sapiens"
		/db_xref="taxon:9606"
		/clone="IMAGE:3060080"
		/clone_1ib="NIH_MGC.37"
		/tissue_type="lymph"
		/cell_type="germinal center B cells"
		/cell_line="MGC85"
		/lab_host="DH10B (LTR)"
		/note="Vector: pUT73-Pac; Site_1: NotI; Site_2: Eco RI;
		Constructed from size fractionated cytoplasmic mRNA
		(1.5-2.5kb). Directionally cloned. Cells provided by Louis
		M. Staudt, Ph.D. Library preparation by Maria de Fatima
		Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT	103 a 122 c 114 g 105 t	
ORIGIN		
Query Match	31.2%; Score 227.2; DB 90; Length 444;	
Best Local Similarity	79.8%; Pred. No. 1e-57;	
Matches 268; Conservative	0; Mismatches 68; Indels 0; Gaps 0;	
Oy	394 gatgttttgatgaccacaactccactcacttctgtcgtttaccattgsgacaacagcctcc	453
Db	6 GGATGAGGAGATGACATCACTCCACTCCCTCCGCCCTGACACCTTGAGACACCGCGCTCC	65
Oy	454 atctcttgcagtgcaagtcagagcctcttgatagtgtatgtaagaagcattattgattgg	513
Db	66 ATCTCTCTCAGAGTCTAGTCAAAAGCCTCCACACACATGATGGAACCACTTACTTGAAATGG	125
Oy	514 ttgttagcagatgcccagcgccagctctccacaagcgcccaatctatctgtgtctcaaacatgg	573
Db	126 TTTTCAGCAGAGGCCAAGGCCAATCTCCAAATGAGCCTTAATTATTAAGGTTTCTAACCGGAC	185
Oy	574 tctggaagctccctgacaggttcaactgacgttgatgacaggaacagatttcacactgaanaatc	633
Db	186 TCTGGGGTCCCAAGACAGATTCCAGCGCGAGTGGGTCCAGCAGCTGACTTCACACTGAAATTC	245
Oy	634 aacagagatgtaggcctgaagatttggagatttatattgtctgtcgaaggtacacattctccg	693

BASE COUNT	88 a	114 c	111 g	112 t
ORIGIN	M.Felima RONALDO.			
Query Match	30.6%	Score 223.4;	DB 24;	Length 425;
Best Local Similarity	78.9%;	Pred. No. 1.4e-56;		
Matches 266;	Conservative 0;	Mismatches 71;	Indels 0;	Gaps 0
393	ggatgttttgatgaccacacccacactcttgcgtgtaccattgacacacagctc 452			

Db 80 GGATATTGTATGACTGACTGCTCCACTCTCCCGCCCGTACATCCCTGGAGACCGGCTC 139  
 Qy 453 catctcttgcaggtaagtcagaagcctctgtagatagtgaagaacatatltgaattg 512  
 Db 140 CATCTCTCTGCAGACTGTAGTCAGAGCCCTCCGCTAGTAATGATTAATATTATTGGATTG 199  
 Qy 513 gtgttcacaagggccaagccagctctccaaagggcccaactctctcgtgtctaaacttga 572  
 Db 200 GTATCTGTGAGAGGACAGAGGCGATGCTCCACAGCCTCCGATCTATTGTGGCTTCAATGGGCG 259  
 Qy 573 ctctgcgaagctccctacacaggttcactctggaatgtatccaaggaagatlltcacactgaaat 632  
 Db 260 CTCGGGGGTCCCTCAGAGGTTCAAGTGCATGTGATCAGGACGACAGATTATTACACTGAAAT 319  
 Qy 633 caacaaagtctgaaggtctgaagatlttggagtttatcttctctgccaagtgacaactctcc 692  
 Db 320 CAGCAGAGTGGAGGCTCAGAGATGTTGGGGTTTTCACCTCATGACGAGGCTCTCAATCTCC 379  
 Qy 693 gctcacgtctggtctgcgcaccaaactcgtgaatactcaa 729  
 Db 380 TCACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA 416

RESULT	9						
AA405415							
LOCUS	AA405415	442 bp	mrna	EST	09-NOV-1997		
DEFINITION	z55602.1	Soares ovary tumor NbHOT Homo sapiens CDNA clone					
IMAGE:7141987	5'	similar to gb:X72467	IG KAPPA CHAIN PRECURSOR	V-IL			
REGION (HUMAN):		mrna sequence.					

ACCESSION	AA405415
VERSION	AA405415.1
KEYWORDS	GI:20636522
SOURCE	EST.
ORGANISM	human. Homo sapiens

REFERENCE  
AUTHORS

Eumariota: Metazoa: Chordata: Cranista: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homiinae: Homo.  
1 (bases 1 to 442)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Giesel, G., Jost, S.,

**TITLE** Mashu-NCI human EST project  
**JOURNAL** Unpublished (1997)  
**COMMENT** Contact: Wilson RK

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [estwatson.wustl.edu](mailto:estwatson.wustl.edu)  
This clone is available royalty-free through LILU; contact the  
IMAGE Consortium ([info@image.lil.lu](mailto:info@image.lil.lu)) for further information.  
Insert length: 1053 Std Error: 0.00  
Seq primer: -28ml3 rev2 ET from Amerisham.

## FEATURES

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/organism="Homo sapiens"
/db_xref="GDB:5942254"
/db_xref="taxon:9606"
/clone_image="741987"
/clone_lib="Scares ovary tumor NdhOT"
/sex="female"
/tissue_type="Ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: ovary; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'-
TGTTACCATCTGGAAGTGGGCGCCGCGGGGTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
A.Fátima Bonaldo."

```

BASE COUNT	90 a	120 c	114 g	118 t
ORIGIN				

Query Match	30.68;	Score 223.4;	DB 7;	Length 442;
Best Local Similarity	78.98;	Pred. No. 1.4e-56;		
Matches 266;	Conservative	0;	Mismatches 71;	Indels 0;
				Gaps 0

Oy 393 gggttttggtagcccaaatcactcacttcttggttacacttgacacacagctc 452  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 80 GGATATTGTATGACTCACTGCTCCACTTCCTCCCTCCGCTATCCTTGAGGCCGGCTC 139  
 Oy 453 catctcttgcacgtcaagtcacagaccctcttgatagatgatgaaagacatattgtaatg 512  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 140 CATCTCCGCGAAGCTTAGTCAAGACCCTCCTCTTAGTAATGGAATATATTATTGGATTG 199  
 Oy 513 gtgttacaagagccagagccagctcttcacaaagccctaactatctatctgtgtctaaacttga 572  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 200 GTATGTGAGAGAGCAGGGCAGTGTCCACAGCTCTGATGTATTGGGTTCTATCGGC 259  
 Oy 573 ctcttgagtccttcacagagttcacttgtagtgatgcagagacagattcacactgaaat 632  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 260 CTCGGGGGTCCCTCAGACAGTTCACTGGCAGTGATCAGGACACAAATTTTACACTGAAAT 319  
 Oy 633 caacagagttgaagctcgaagatttgggaattatattgctctggaaggtacacattctc 692  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 320 CAGCAGAGTGGAGGCTGAGAGTATGTTGGGTTATCACTGATGCATGCAGGCTCTACATCTCC 379  
 Oy 693 gctcacgttggtgtctgacacacagctggaatacaa 729  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 380 TCACACTTTTGGCCAGGGGACCAAGCTGGAATCAAA 416

RESULT	10
LOCUS	AM405725
DEFINITION	AM405725, 488 bp mRNA, EST 16-FEB-2000
	UT-HR-BE0-abv-f-05-0-UT1 NIH_MGC_37 Homo sapiens cdNA clone
	IMAGE:3057944 5', mRNA sequence.

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
AM405725.	AM405725.1	GI:6924782	EST.	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	1 (bases 1 to 488)	NIH-MGC <a href="http://www.ncbi.nlm.nih.gov/MGC/">http://www.ncbi.nlm.nih.gov/MGC/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC)
					unpublished (1999)	Contact: Robert Strausberg, Ph.D.			

Tel.: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Eco RI site shown at the beginning of the sequence.  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: M.B. Soares Lab  
 cDNA Library Arrayed by: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/BLN at:  
[www.bio.lnl.gov/bcrr/image/image.html](http://www.bio.lnl.gov/bcrr/image/image.html)  
 seq primer: M3 forward.

FEATURES,	Location/Qualifiers
source	1. .488

```

"organism"="Homo sapiens"
"db_xref"="taxon:9606"
"clone_image"="3057944"
"clone_lib"="NIH_MGC_37"
"tissue_type"="lymph"
"cell_type"="germinal center B cells"
"cell_line"="MGC85"
"lab_host"="DH10B (LTR)"
"note"="Vector: pUT73-Pac; Site_1: NotI; Site_2: Eco RI"
Constructed from size fractionated cytoplasmic mRNA

```





REFERENCE 1 (bases 1 to 911)  
 AUTHORS NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: Lohar Hennighausen Ph.D., Robin Humphreys  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)  
 DNA Sequencing by: Incey Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>  
 Plate: LHAM524 row: k column: 18  
 High quality sequence stop: 688.

## FEATURES

source

1. .911  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /strain="C57/B6"  
 /db\_xref="taxon:10090"  
 /clone\_lib="IMAGE:3487241"  
 /clone\_lib="NCI\_CGAP\_Mam5"  
 /tissue\_type="tumor, gross tissue"  
 /dev\_stage="7 months"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: Salt; Site\_2: Not; Cloned unidirectionally. Primer: oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lohar Hennighausen/Robin Humphreys, NIH"

BASE COUNT 190 a 262 c 261 g 197 t 1 others  
 ORIGIN

Query Match 29.5%; Score 214.8; DB 106; Length 911;  
 Best Local Similarity 79.2%; Pred. No. 7.2e-54;  
 Matches 282; Conservative 0; Mismatches 67; Indels 7; Gaps 2;

QY 1 caggctgacgtcagcagctctggggcagagcctgtgagtcagggcctcagtcagttg 60  
 |||||  
 DB 65 CAGGTCACATGACGACGCGCTGGGGCTGTGAGAGCTGGGCTTACGAAACCTG 124  
 |||||  
 QY 61 tctctgacagctctgtgctcaacatgaagactatgacgtggtgaa-gcagag 119  
 |||||  
 DB 125 TCCTGCAGGCTTCTGCTACACCTTACCAAGTTACTGATGCACTGGGTGAACGCAAG 184  
 |||||  
 QY 120 gcctgacagggcctggagtgagttgagttgacccctgagaatgtgatactgata 179  
 |||||  
 DB 185 GCCTGGACGAGGCTTGAAGGATGATGATGATGATGATGATGATGATGATGATGAT 244  
 |||||  
 QY 180 tgcctgacaggtcagggcagagcctcagtcagtcagtcagtcagtcagtcagtc 229  
 |||||  
 DB 245 CAATGAGAACTTCAAGGACGACACCTGATGAGAAACCCCTCGACGACGACTA 304  
 |||||  
 QY 240 cctgagagtcagagcctgcatctgagacactgacccgtctattatgtatattttac 299  
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 DB 305 CATGCAAGCTGAGAGCTGATGAGAGCTGCGGTATTAATTAATTAATTAATTAAT 364  
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 QY 300 ggaat-----gcttgactacttgaggcacaaggagcagtcacgctcctcag 349  
 |||||  
 DB 365 GGATTAGAGAGCTATGAGACTGAGGCTCAAGAACTCAGTCAAGCTCTCCACAG 420  
 |||||

RESULT 15  
 AM406473 353 bp mRNA EST 16-FEB-2000  
 LOCUS UI-HF-B10-act-e-08-0-UI.1 NIH\_MGC\_37 Homo sapiens cDNA clone  
 DEFINITION IMAGE:3060182 5', mRNA sequence.  
 ACCESSION AM406473  
 VERSION AM406473.1 GI:6925530

KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 353)  
 AUTHORS NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Eco RI site shown at the beginning of the sequence.  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 CDNA Library Preparation: M.B. Soares Lab  
 CDNA Library Arrayed by: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: [www.bio.lnl.gov/bdrp/image/image.html](http://www.bio.lnl.gov/bdrp/image/image.html)  
 Seq primer: M13 forward.

## FEATURES

source

1. .353  
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 /db\_xref="taxon:9606"  
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 /tissue\_type="lymph"  
 /cell\_type="germinal center B cells"  
 /cell\_line="Mc85"  
 /note="Vector: p7773-Pac; Site\_1: Not; Site\_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 73 a 93 c 93 g 94 t  
 ORIGIN

Query Match 29.3%; Score 213.4; DB 90; Length 353;  
 Best Local Similarity 80.4%; Pred. No. 1.4e-53;  
 Matches 250; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 393 ggaatgtttgatacccaactccactcacttctgtggttaccattggacaacagcctc 452  
 |||||  
 DB 43 GGATATTGTAATACACAGCTCAGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 102  
 |||||  
 QY 453 catctctgcaagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 512  
 |||||  
 DB 103 CATCTCTCAGAGCTGATGAGAGCTCCTGCAATGATGATGATGATGATGATGATGATG 162  
 |||||  
 QY 513 gtgttaccagggcagggcagtcctcagtcagtcagtcagtcagtcagtcagtcagtc 572  
 |||||  
 DB 163 GTACCTGACAGAGCCAGGAGCTCAGAGCTCCTGATCTATTTGTTCTAATGGGCG 222  
 |||||  
 QY 573 cctctgagtcctcagaggttcagtcagtcagtcagtcagtcagtcagtcagtcagtc 632  
 |||||  
 DB 223 CTCGGGGGTCCTGAGAGGTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 282  
 |||||  
 QY 633 caacagagtgagagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 692  
 |||||  
 DB 283 CACCAAGAGGAGAGGATGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 342  
 |||||  
 QY 693 gctcagcttcg 703  
 |||||  
 DB 343 TCTCACTTCG 353

Search completed: February 18, 2001, 02:00:11  
 Job time: 13895 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 17, 2001, 18:26:59 ; Search time 96.92 seconds

(without alignments)  
2825.610 Million cell updates/sec

Title: US-09-297-181-1

Perfect score: 729  
Sequence: 1 caggtgcagctgcagcagc.....gcaccagctggaatcaaa 729

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_36:\*

- 1: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1980.DAT:\*
- 2: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1981.DAT:\*
- 3: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1982.DAT:\*
- 4: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1983.DAT:\*
- 5: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1984.DAT:\*
- 6: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1985.DAT:\*
- 7: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1986.DAT:\*
- 8: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1987.DAT:\*
- 9: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1988.DAT:\*
- 10: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1989.DAT:\*
- 11: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1990.DAT:\*
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- 19: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1998.DAT:\*
- 20: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1999.DAT:\*
- 21: /cgn2\_2/gcgdata/geneseq/geneseqn/NA2000.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	729	100.0	729	19	V36236 DNA of SCFV 421 wh
2	717.8	98.5	768	17	T48000 Coding sequence fo
3	716.2	98.2	749	18	T86234 Anti-human protein
4	716.2	98.2	1611	18	T86234 Human p53 protein
5	505	69.3	1135	20	X58936 Plasmid pUG718 enc
6	460.8	63.2	747	19	V36237 DNA of SCFV D3M wh
7	452.2	62.0	1314	19	V09256 Nucleotide sequen
8	435	59.7	907	20	X58690 Monoclonal antibody
9	432.2	59.3	753	20	X77245 Mouse scfv fragmen
10	432.2	59.3	810	16	O90663 MFE-23 antibody co
11	432.2	59.3	1637	21	Z88558 Bispesific anti-ze
12	429	58.8	753	20	X77241 Mouse scfv fragmen

13	425.2	58.3	1679	18	T58130
14	425.2	58.3	1679	20	V08176
15	418	57.3	726	20	X86942
16	418	57.3	726	20	X86943
17	415.2	57.0	843	20	V72069
18	415.2	57.0	1998	20	V72075
19	409.4	56.2	830	21	T61047
20	407.4	55.9	1095	18	T94969
21	407.4	55.9	1098	18	T94970
22	405.8	55.7	876	19	V10390
23	393	53.9	925	21	Z58664
24	393	53.9	925	21	Z44206
25	392	53.8	1047	20	Z21156
26	392	53.8	1086	20	Z21158
27	385.2	52.8	804	20	X78155
28	377.4	51.8	864	20	V72072
29	377.4	51.8	2019	20	V72059
30	377.4	51.8	2025	20	V72064
31	368.8	50.6	744	20	X77247
32	361.8	49.6	772	14	O35954
33	361.8	49.6	772	17	T27991
34	361.8	49.6	778	14	O35955
35	360.8	49.5	744	20	X77248
36	357.6	49.1	744	20	X77243
37	356.8	48.9	1725	20	X01651
38	354.8	48.7	732	19	V23579
39	354.8	48.7	2364	19	V23580
40	352.6	48.4	2478	20	X86614
41	352.6	48.3	720	19	V54790
42	351.6	48.2	747	13	O21098
43	349.2	47.9	1668	20	X01652
44	349.2	47.9	1797	19	V00687
45	349.2	47.9	1797	21	A10398

#### ALIGNMENTS

RESULT 1

V36236

ID V36236 standard: DNA; 729 BP.

XX V36236;

AC XX

DT 08-SEP-1998 (first entry)

DE DNA of SCFV 421 which binds to mutant p53 proteins.

XX

XX Single chain antibody; SCFV 421; mouse; p53 protein; oligomerisation;

KW regulatory domain; p53 mutant; H273; W248; G281;

KW p53-dependent trans-activating activity; restoration;

KW tumour-suppressing activity; tumour cell; treatment;

XX hyper-proliferation; cancer; re-stenosis; ss.

XX

OS Mus sp.

XX

PN W0918825-A1.

XX

PD 07-MAY-1998.

XX

PF 27-OCT-1997; 97MO-FR01921.

XX

PR 29-OCT-1996; 96FR-0013176.

XX

PA (RHON) (RHON)-POUDENC RORER SA.

XX

PI Debussche L, Bracco L;

XX

DR WPI: 1998-272140/24.

DR P-PSDB; W60769.

XX

XX Restoring p53-dependent trans-activating activity to cell containing

PT mutant p53 - by delivering single-chain antibody specific for the

PT mutant, particularly for treatment of tumours  
 XX  
 PS Claim 5; Page 31; 54pp; French.  
 XX

CC The present sequence encodes a single chain antibody (SCFV) designated  
 CC 421. The antibody binds to an epitope present in the C-terminal region  
 CC of the p53 protein that includes oligomerisation and regulatory domains,  
 CC specifically between positions 320 and 393. SCFV 421 is directed against  
 CC p53 mutants, particularly H273, W248 and G281 mutants. When the SCFV is  
 CC introduced into cells containing a mutant p53 protein, p53-dependent  
 CC trans-activating activity is restored. SCFV 421 is specific for  
 CC p53-mutants that have lost tumour-suppressing activity and are present in  
 CC tumour cells. It is particularly used to treat hyper-proliferation  
 CC associated with these mutants (e.g. cancer and re-stenosis) but may also  
 CC be used in vitro for studying mechanisms of activity of p53 or its mutant  
 CC and to purify or detect p53.  
 CC  
 XX

SQ Sequence 729 BP; 174 A; 171 C; 207 G; 177 T; 0 other;

Query Match 100.0%; Score 729; DB 19; Length 729;  
 Best Local Similarity 100.0%; Pred. No. 2, 4e-200;  
 Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagtgcaagctgcaagctctgaggaagcttgtaaggaagggcctcagcaagt 60  
 DB 1 caagtgcaagctgcaagctctgaggaagcttgtaaggaagggcctcagcaagt 60  
 QY 61 tccgcgcaagcttctgcttaacataaagactactatagcactgggtgaagcagg 120  
 DB 61 tccgcgcaagcttctgcttaacataaagactactatagcactgggtgaagcagg 120  
 QY 121 cctgaacagagcctcgagatgagtgatctatcctcgaggaatggtgaacagaa 180  
 DB 121 cctgaacagagcctcgagatgagtgatctatcctcgaggaatggtgaacagaa 180  
 QY 121 cctgaacagagcctcgagatgagtgatctatcctcgaggaatggtgaacagaa 180  
 DB 121 cctgaacagagcctcgagatgagtgatctatcctcgaggaatggtgaacagaa 180  
 QY 181 gccccgaagctcagaggaagcactatgactgagacacatcctccataacagcc 240  
 DB 181 gccccgaagctcagaggaagcactatgactgagacacatcctccataacagcc 240  
 QY 241 ctgagagctcagacagcctgagcactgaggaagcctgctcttcttgaattta 300  
 DB 241 ctgagagctcagacagcctgagcactgaggaagcctgctcttcttgaattta 300  
 QY 241 ctgagagctcagacagcctgagcactgaggaagcctgctcttcttgaattta 300  
 DB 241 ctgagagctcagacagcctgagcactgaggaagcctgctcttcttgaattta 300  
 QY 301 gatccttgagcacttggggcgaagggcagccaggtcaccgctcctcctcaggt 360  
 DB 301 gatccttgagcacttggggcgaagggcagccaggtcaccgctcctcctcaggt 360  
 QY 301 gatccttgagcacttggggcgaagggcagccaggtcaccgctcctcctcaggt 360  
 DB 301 gatccttgagcacttggggcgaagggcagccaggtcaccgctcctcctcaggt 360  
 QY 361 tcaagcgagaggtgctcctgctgctgagcgatcgatgtttgatgacccaactc 420  
 DB 361 tcaagcgagaggtgctcctgctgctgagcgatcgatgtttgatgacccaactc 420  
 QY 361 tcaagcgagaggtgctcctgctgctgagcgatcgatgtttgatgacccaactc 420  
 DB 361 tcaagcgagaggtgctcctgctgctgagcgatcgatgtttgatgacccaactc 420  
 QY 421 acttgctggttaccatttggaacacccagcctcctcttcttgaagttaagcag 480  
 DB 421 acttgctggttaccatttggaacacccagcctcctcttcttgaagttaagcag 480  
 QY 421 acttgctggttaccatttggaacacccagcctcctcttcttgaagttaagcag 480  
 DB 421 acttgctggttaccatttggaacacccagcctcctcttcttgaagttaagcag 480  
 QY 481 ttgagatgctgtaagaagacacatttgaattggtttacagagagccagccact 540  
 DB 481 ttgagatgctgtaagaagacacatttgaattggtttacagagagccagccact 540  
 QY 481 ttgagatgctgtaagaagacacatttgaattggtttacagagagccagccact 540  
 DB 481 ttgagatgctgtaagaagacacatttgaattggtttacagagagccagccact 540  
 QY 541 aagcgctaatatctatctggtgtctaaactggactctgagtcctgacaggtt 600  
 DB 541 aagcgctaatatctatctggtgtctaaactggactctgagtcctgacaggtt 600  
 QY 541 aagcgctaatatctatctggtgtctaaactggactctgagtcctgacaggtt 600  
 DB 541 aagcgctaatatctatctggtgtctaaactggactctgagtcctgacaggtt 600  
 QY 601 agtgcagcaggaagacatttcaacactgaacacagagtgagggtctgagatt 660  
 DB 601 agtgcagcaggaagacatttcaacactgaacacagagtgagggtctgagatt 660  
 QY 601 agtgcagcaggaagacatttcaacactgaacacagagtgagggtctgagatt 660  
 DB 601 agtgcagcaggaagacatttcaacactgaacacagagtgagggtctgagatt 660  
 QY 661 gttattattctgcaagagtaacacattcctcgctcaagttcgggtcgacacaag 720  
 DB 661 gttattattctgcaagagtaacacattcctcgctcaagttcgggtcgacacaag 720  
 QY 661 gttattattctgcaagagtaacacattcctcgctcaagttcgggtcgacacaag 720  
 DB 661 gttattattctgcaagagtaacacattcctcgctcaagttcgggtcgacacaag 720  
 QY 721 gaatacaaa 729

DB 721 gaatacaaa 729

RESULT 2

T48000

ID T48000 standard; CDNA; 768 BP.

AC T48000;

DT 10-JUN-1997 (first entry)

DE Coding sequence for single-chain antibody to the p53 protein.

XX Chimeraic; bispecific; DNA binding domain; trans: activator; repressor;

XX diptheria; Pseudomonas; toxin; thymidine kinase; single chain antibody;

XX pathogen; HIV Tat; papilloma virus; E6/E7; Epstein-Barr virus; EBNA;

XX hyperproliferation; p53; tumour; oligomerisation; ss.

XX Synthetic.

XX W09630512-A1.

XX 03-OCT-1996.

XX 29-MAR-1996; 96MO-FR00477.

XX 31-MAR-1995; 95FR-0003841.

XX (RHON) RHONE-FOULENC ROBER SA.

XX Bracco I, Schweighoffer F, Tocque B;

XX WPI; 1996-45359/45.

XX Conditional gene expression system triggered by e.g. infection or

XX hyper-proliferation - comprises novel bi-specific proteins having

XX DNA-binding domain and second domain specific for trans-activator or

XX repressor, for gene therapy

XX Claim 53; Page 44-45; 81pp; French.

XX The invention relates to novel chimeraic, bispecific proteins which

XX comprise: (a) a DNA binding domain and (b) a domain which binds a

XX trans-activator (TA), trans-repressor (TR) or their complexes, which are

XX characteristic of a physiological or pathological state. The novel

XX chimeraic, bispecific proteins allow expression of a therapeutic protein

XX (e.g. diptheria or pseudomonas toxins, thymidine kinase, single chain

XX antibodies) to be regulated in response to particular conditions.

XX The TA- or TR-binding domain may be a antibody such as a single chain

XX antibody. This sequence encodes such a single chain antibody targeted

XX to the p53 protein. The sequence is constructed from the gene encoding

XX the light and heavy chain variable regions of the antibody produced by

XX hybridoma pnb421. The 340 and 325 bp sequences encoding the heavy and

XX light chain variable regions respectively are amplified by PCR and

XX linked together by a linker "arm". In the protein produced (sequence

XX not given in the specification), amino acids 9-241 represent the linked

XX V-linker-VI sequence. The protein also contains an myc epitope tag

XX represented by amino acids 256-266.

XX

SQ

-Sequence 768 BP; 181 A; 185 C; 218 G; 184 T; 0 other;

Query Match 98.5%; Score 717.8; DB 17; Length 768;

Best Local Similarity 99.0%; Pred. No. 4e-197; 7; Indels 0; Gaps 0;

Matches 722; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 caagtgcaagctgcaagctctgaggaagcttgtaaggaagggcctcagcaagt 60

DB 28 caagtgcaagctgcaagctctgaggaagcttgtaaggaagggcctcagcaagt 87

QY 61 tccgcgcaagcttctgcttaacataaagactactatgactgggtgaagcagg 120

DB 1 tccgcgcaagcttctgcttaacataaagactactatgactgggtgaagcagg 120



QY 541 aagcgccatctatctgtgtcttcaactgagctgtgagctccctgacaggttcaactgagc 600  
 |||||  
 Db 550 aagcgccatctatctgtgtcttcaactgagctgtgagctccctgacaggttcaactgagc 609  
 QY 601 agtgcatacagggagacagatttcaacactgaaatacaacagagtgaggtgagattggga 660  
 |||||  
 Db 610 agtgcatacagggagacagatttcaacactgaaatacaacagagtgaggtgagattggga 669  
 QY 661 gttattatctgcgcagaggtacacattctcgcctcagcttgcgtgctgagacccaagctg 720  
 |||||  
 Db 670 gttattatctgcgcagaggtacacattctcgcctcagcttgcgtgctgagacccaagctg 729  
 QY 721 gaaatcaaa 729  
 |||||  
 Db 730 gagctgaaa 738  
 RESULT 4  
 ID T86221 standard; cDNA; 1611 BP.  
 AC T86221;  
 DT 24-NOV-1997 (first entry)  
 DE Human p53 protein variant S-325 coding sequence from pEC176.  
 XX  
 KM Leucine zipper domain; LZD; oligomerisation domain; mutant; mutleu;  
 KM substitution; replacement; transactivation; viral protein VP16; HSV;  
 KM anti-oncogene; hyperproliferation; cancer; restenosis; SCFV;  
 KM tumour suppression; apoptosis; single chain antibody variable domain;  
 KM SS.  
 XX  
 OS Chimeric - Homo sapiens.  
 OS Chimeric - Herpes simplex virus.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1611  
 FT /\*tag- a  
 FT /product- S-325  
 FT /note- "Open reading frame ends with two tandem  
 termination codons"  
 FT  
 PN MO9704092-A1.  
 PD 06-FEB-1997.  
 PF 17-JUL-1996; 96WO-FR01111.  
 PR 19-JUL-1995; 95FR-0008729.  
 XX  
 PA (RHON ) RHONE POULENC ROBER SA.  
 XX  
 PI Bracco L, Conseiller E;  
 XX  
 DR WPI; 1997-132633/12.  
 XX P-PSDB; W28491.  
 PT New p53 variants e.g. with oligomerisation domain replaced by  
 leucine zipper - useful for treating hyper-proliferative disorders,  
 esp. cancer and restenosis  
 XX  
 PS Claim 42; Pages 88-90; 133pp; French.  
 CC Claimed variants of protein p53 have at least part of the  
 CC oligomerisation domain deleted and replaced by a leucine zipper  
 CC domain. The mutants preferably also have at least part of the p53  
 CC transactivation domain (amino acids 1-74) deleted and replaced by  
 CC the transactivating domain (TD) from herpes simplex virus viral  
 CC protein VP16 (amino acids 411-490) or by a protein domain able to  
 CC bind selectively to a transactivator, especially a single-chain

CC antibody variable domain (SCFV). The present sequence encodes  
 CC a specifically claimed-p53 variant designated S-325 and comprising  
 CC a SCFV domain, amino acids 75-325 of human wild-type p53 and a  
 CC leucine zipper domain at the C-terminal. The p53 variants are  
 CC more active and more stable tumour suppressors and apoptosis-inducing  
 CC agents than wild-type p53 and are active where the wild-type protein  
 CC is not, i.e. they are not inactivated by dominant negative or oncogenic  
 CC mutants, nor by other cellular proteins (because the leucine zipper  
 CC domain prevents formation of inactive mixed oligomers).  
 XX  
 SQ Sequence 1611 BP; 369 A; 443 C; 458 G; 341 T; 0 other;

Query Match 98.2%; Score 716.2; DB 18; Length 1611;  
 Best Local Similarity 98.9%; Pred. No. 1.5e-196;  
 Matches 721; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 caggtgcagctgcagcagctctggggcagagctgtgagtcaggggcctcaagcttg 60  
 |||||  
 Db 7 caggtgcagctgcagcagctctggggcagagctgtgagtcaggggcctcaagcttg 66  
 QY 61 tcttcgacagctctgcgttcacattaaagactactatgtgactgggtgagcagag 120  
 |||||  
 Db 67 tcttcgacagctctgcgttcacattaaagactactatgtgactgggtgagcagag 126  
 QY 121 cctgaacagggcctggagtgatgtgattgattcctcgtgagattgtgataat 180  
 |||||  
 Db 127 cctgaacagggcctggagtgatgtgattgattcctcgtgagattgtgataat 186  
 QY 181 gccccgaagttccagggcagggccactatgactgcagacacatcccaatacagcttac 240  
 |||||  
 Db 187 gccccgaagttccagggcagggccactatgactgcagacacatcccaatacagcttac 246  
 QY 241 ctgcagctcagcagcctgcgcatctgagagacactgcgcctctattgttaatttttcaggg 300  
 |||||  
 Db 247 ctgcagctcagcagcctgcgcatctgagagacactgcgcctctattgttaatttttcaggg 306  
 QY 301 gatgcttggactattggggcagaggacacagtcacgctcctcctcaggtgagggcgt 360  
 |||||  
 Db 307 gatgcttggactattggggcagaggacacagtcacgctcctcctcaggtgagggcgt 366  
 QY 361 tcagcggagagtgctgcctgcggtgagcagatcgatgatttgatgagcccaactcac 420  
 |||||  
 Db 367 tcagcggagagtgctgcctgcggtgagcagatcgatgatttgatgagcccaactcac 426  
 QY 421 acttgcgttacacattgagcaacagcctccatctcttgcaggtcaggtcagcctc 480  
 |||||  
 Db 427 acttgcgttacacattgagcaacagcctccatctcttgcaggtcaggtcagcctc 486  
 QY 481 ttgataagtgatggaagacatatattgaattggtgttacaagggccaggccagcttcca 540  
 |||||  
 Db 487 ttgataagtgatggaagacatatattgaattggtgttacaagggccaggccagcttcca 546  
 QY 541 aagcgccatctatctgtgtgttaactgagctctgaggtccctcaaggttcaactgagc 600  
 |||||  
 Db 547 aagcgccatctatctgtgtgttaactgagctctgaggtccctcaaggttcaactgagc 606  
 QY 601 agtgcatacagggagacatttcaacactgaaatacaacagagtgaggtgagattggga 660  
 |||||  
 Db 607 agtgcatacagggagacatttcaacactgaaatacaacagagtgaggtgagattggga 666  
 QY 661 gttattatctgcgcagaggtacacattctcgcctcagcttgcgtgctgagacccaagctg 720  
 |||||  
 Db 667 gttattatctgcgcagaggtacacattctcgcctcagcttgcgtgctgagacccaagctg 726  
 QY 721 gaaatcaaa 729  
 |||||  
 Db 727 gagctgaaa 735  
 RESULT 5  
 ID X58936 standard; DNA; 1135 BP.

[illegible]

QY	122	ctgaaacaggcgctggaatggatggatggatggtatgctctggaagtgtggtatcaggaatg	181
Db	306	atggaaagagatcttgagctggaatcgtggaataataatccctactctatgtgaatactagcctaa	365
QY	182	ccccgaagttccaaaggcgaaagcccaactgactgcagacaacatcctccaataacagcctaac	241
Db	366	atccgaagttcaagatcgaaaggccaccatctgctctgaagcaaatcttccagacagcctaac	425
QY	242	tgcaagctcaagcagcctgagcatctgaaaggacaactgcgctatattgt-----	288
Db	426	tgcaagctcaaaagatcagatctgaaaggacctcgacgtcacttactctgtaagaggatt	485
QY	289	-----aatcttlaagggatgagctttgcaactatttgaggcgcaaggacaacagctgaacg	340
Db	486	attactacgtagaagctlaagcagagcgcttccctactgaggcgcaaggacccctgctacg	545
QY	341	tctactcaagtgagagcgaggttcacagcgagagtggtctctcggttgcggaatcgatgatt	400
Db	546	tctctgcaaggggtggtgcggtcccggaaggatggcagcggaggggcgagctccgattgtg	605
QY	401	tgatgataccaaactccactcaactttgcggttaccatctggaacaacagcctcatctct	460
Db	606	tgatgatacccaagctccactcaactttgctgacttaacattggaacaacagcctcatctct	665
QY	461	gcaagttcaagtcacaagcgtctctggaatgatagtatgaaagaacatatcttgaattggtttac	520
Db	666	gcaagttcaagtcacaagcgtctcttgaatgatagtatgaaagaacatatcttgaattggtttac	725
QY	521	agagggccagcgccagctctcccaaaagcgccatactcaactcgtgcgtcctaaactggaactggag	580
Db	726	agagggccagcgccagctctcccaaaagcgccatactcgtgcgtcctaaactggaactggag	785
QY	581	tcctctgaaggtttactctgcaatgtagatcagaggagacagattccaactgaaaaatacaacagag	640
Db	786	tcctctgaaggtttactctgcaatgtagatcagaggagacagattccaactgaaaaatacaacagag	845
QY	641	tgaggagctcgaagatttgaggagatttatattgttcgtgcagagttacacattcccgctacgt	700
Db	846	tgaggagctcgaagatttgaggagatttatattgttcgtgcagagttacacattcccgcaagct	905
QY	701	tcgggtgctgtagcaccacaagctggaatacaaa	729
Db	906	tcgggtgtaggaccacaagctggaatacaaa	934
RESULT	6		
ID	V36237		
XX	V36237 standard; DNA; 747 BP.		
AC	V36237;		
XX	08-SEP-1998 (first entry)		
DT			
DE	DNA od SCFV D3M;which binds to mutant p53 proteins.		
KW	Single chain antibody; SCFV D3M; mouse; p53 protein; oligomerisation;		
KW	regulatory domain; p53 mutant; H273; W248; G281;		
KW	p53-dependent trans-activating activity; restoration;		
KW	tumour-suppressing activity; tumour cell; treatment;		
KW	hyper-proliferation; cancer; re-stenosis; ss.		
OS	Mus sp.		
XX	WO9818625-A1.		
XX	07-MAY-1998.		
XX	27-OCT-1997; 97MO-FR01921.		
XX	29-OCT-1996; 96FR-0013176.		
XX	(RHON ) RHONE-PJULENC RORER SA.		

Pt	Debusche L, Bracco L;
Xx	MPI: 1998-272140/24.
DR	F-PSDB: W60770.
Xx	Restoring p53-dependent trans-activating activity to cell containing
Pt	mutant p53 - by delivering single-chain antibody specific for the
Pt	mutant, particularly for treatment of tumours
Xx	Claim 5; Page 32; 54pp; French.
Ps	
Cc	The present sequence encodes a single chain antibody (scFv) designated
Cc	D3M. The antibody binds to an epitope present in the C-terminal region
Cc	of the p53 protein that includes oligomerisation and regulatory domains,
Cc	specifically between positions 320 and 393. scFv D3M is directed against
Cc	p53 mutants, particularly H273, W248 and G281 mutants. When the scFv is
Cc	introduced into cells containing a mutant p53 protein, p53-dependent
Cc	trans-activating activity is restored. scFv D3M is specific for
Cc	p53-mutants that have lost tumour-suppressing activity and are present in
Cc	tumour cells. It is particularly used to treat hyper-proliferation
Cc	associated with these mutants (e.g. cancer and re-stenosis) but may also
Cc	be used in vitro for studying mechanisms of activity of p53 or its mutant
Cc	and to purify or detect p53.
Cc	
Xx	Sequence 747 BP; 189 A; 188 C; 205 G; 165 T; 0 other;
SO	
Query Match	63.2%; Score 460.8; DB 19; Length 747;
Best Local Similarity	79.2%; Pred. No. 3, 2e-123;
Matches 594; Conservative	0; Mismatches 132; Indels 24; Gaps 3
Oy	1 cagggtgcacgttcagcaagctctgggctgggaagagcttgtaagtcaggggccctaagtcagt 60
Dd	
Oy	1 caggtcaacctcgacaggaagtcagggaagaactctgtgaagtcaggggccctaagtcattg 60
Oy	61 tccctgcacagctctcttgctccaacatcaaaagactactatatatgcactcgggtggaaacagag 120
Dd	61 tccctgcacagctctcttgctccaacatcaaaagactactatatatgcactcgggtggaaacagag 120
Oy	121 cctgcacaaggagccttggaagtgtgatctgtgatcatcctctggaaatgtgtatactgatat 180
Dd	121 cctgcagaagagcgcttgtagtgatctgtgatctgtgatcatcctctggaaatgtgtatactgatat 180
Oy	181 gcccccgaagttccaaagggcaaagccactatgatctgcagacaacatcctccaatcacgccctac 240
Dd	181 gcccccgaacctccaagggcaaagccactatgtgactctgcagacaacatcctccaacacagcctac 240
Oy	241 ctgcagagtcagaagaccttgaccatcttgaggacaacgctgccttatattgtgtaat----- 291
Dd	241 ctgcagccttcagaagccttgaccatcttgaggacaacacgctccttatattgtatgcagtcacac 300
Oy	292 -----tttacggggaatgctcttggaactatttggggccaagggaccaacggctcacgcgc 342
Dd	301 tactatgaatacagacggcgcatgctcttggaactacttggggccaagggaccaacggcgcacgcgc 360
Oy	343 tccctaagttgagagcggttcacaagcggaaggtgctctgcgtgcgtgvcgagtcgagatgtttcg 402
Dd	361 tccctaagttgagagcggttcacaagcggaaggtgctctgcgtgcgtgvcgagtcgagatgtttcg 420
Oy	403 atgaccaccaaacccaactcaactctgtcgtgtacattggagacaacacgctccacatctcttcg 462
Dd	421 ctcacccaatctccatctctccctgggtgtgtaagcaggagagaaggttcgtctaagagctcgc 480
Oy	463 aagtcacaagtcagacgctctcttga---tagtgtatggaagaacatatttgattgtgttca 519
Dd	481 aaatccagtcacagatctgttccaacagttagaaccocggaagaataattactctgtgttatcgg 540
Oy	520 cagaggtccagagccagatctccaagcgccaatatcatatctgtgttctaanaactgagatcttga 579
Dd	541 cagaacaaccgggacgtctcctaagaagtgctgactctactgtgagcatccactagtggaatcttga 600
Oy	580 gtccctgcagaagttcactgtgcagctgatacagaagacagatttccacactgaaaatacaacaga 639

Dd	601	gtccctgcatcgcttaccagcagcagtgcctggacagattcaacttcaccatcaggcagt	660
Oy	640	gtggagagctgaaggattggagaatttatcttgctggcaaggtcacacaattccgccaa	699
Dd	661	gtgcagagctgtaagacctggcagttacttactycaagcaa--tctataatctaccgacy	717
Oy	700	tccggtgctggcaccacaagctggaaatcca	729
Dd	718	tccggcgggggacccaagctggaatcaaa	747
RESULT	7		
ID	V09256	standard; cDNA; 1314 BP.	
AC	V09256;		
DT	07-JUL-1998	(first entry)	
DE	Nucleotide sequence encoding the Mgr6-clavlin immunotoxin.		
KW	Recombinant ribosomal inhibitor protein; RIP; clavlin; inhibition; ss;		
KM	protein synthesis; conjugate; Mgr6-clavlin; anticancer; antiviral agent		
KX	fusion protein; chimeric.		
OS	Chimeric - Mus musculus.		
OS	Chimeric - Aspergillus clavatus.		
FH	Key	Location/Qualifiers	
FT	CDS	1..1314	
FT		/tag= a	
FT		/product= "Mgr6-clavlin immunotoxin"	
FT	misc-feature	108..861	
FT		/tag= b	
FT		/product= "Single Fv of Mgr6"	
FT		/note= "derived from M. musculus"	
FT	misc-feature	861..1314	
FT		/tag= C	
FT		/product= "Clavlin"	
FT		/note= "derived from A. clavatus"	
Pn	WO9749726-A1.		
Pd	31-DEC-1997.		
Pf	26-JUN-1997;	97WO-EP03359.	
Px	27-JUN-1996;	96IT-FI00155.	
Pr	(TUY-) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.		
Pi	Coinagli M, De Santis R, Mele A, Parente D;		
Px	WPJ: 1998-077105/07.		
Dr	P-PsDB: W377738.		
Pt	DNA encoding Aspergillus clavatus-derived ribosomal inhibitor		
Pt	protein, clavlin. useful as an immuno-conjugate and for treatment of		
Pt	cancer		
Px	Claim 3; Page 13; 26pp; English.		
Px	This nucleotide sequence encodes a fusion protein comprising of the		
Cc	Mgr6 single chain antibody (with the heavy and light chain joined		
Cc	by a linker), fused to the clavlin protein. Clavlin is an inhibitor		
Cc	protein, and functions by inactivating the ribosomes. Clavlin or its		
Cc	conjugates are useful as anticancer and/or antiviral agents. The		
Cc	recombinant ribosomal inhibitor protein (RIP), Mgr6-clavlin (a conjugate		
Cc	of clavlin) is used as an immunoconjugate, and the complex and clavlin		
Cc	alone are capable of inhibiting ribosomal activity.		
Sequence	1314 BP; 338 A; 360 C; 359 G; 257 T; 0 other;		



Accession	Gene	Protein	Species	Length	Start	End	Score	E-value	Identity	Similarity
D6	96	aagcgacgctcggtgagactctcgtggggaagcgctcaagctcgaagcgctggaagcgctcctggaactct	155	1	155	100	0.0	0.0	100	100
Q7	62	ccctgcacaagctcttgctgcttcaacaataaagaactctactatatactgacccgggtgtgaagcagagcg	121	1	121	100	0.0	0.0	100	100
D6	156	cccttgcagagcctccctcggaattcaacttcaactaactcaagcagatgctcttgggttctgcagagctc	215	1	215	100	0.0	0.0	100	100
Q7	122	ctgaacacggccctcggaattgattgatactgattgatccctgaagatggttatactgaatatg	181	1	181	100	0.0	0.0	100	100
D6	216	cagagcaagaagagctcggaattggtctgcacaacattatagaatgatgtgtgtcttcaccccttatgt	275	1	275	100	0.0	0.0	100	100
Q7	182	ccccgaagctcccaagggcagagccactatgaactgcaagacaacatccctccatacagctacc	241	1	241	100	0.0	0.0	100	100
D6	276	cagacacagctgtgaagggcgccgaattccacattcccaagagacatgcccanaaacacccctgtatc	335	1	335	100	0.0	0.0	100	100
Q7	242	tgcagcgccagcagacgctgcacatctgaaggaacacgcgcgctccattatgttaatttttaagggg	301	1	301	100	0.0	0.0	100	100
D6	336	tgcacaatgaacaagcgctgaagatctctggggatctcagagctgattatctgtgttaagagagata	395	1	395	100	0.0	0.0	100	100
Q7	302	atgcctttgcacatcttgggggccaaggggacacagcgctcacgctcctccacaggttgaagcggt	361	1	361	100	0.0	0.0	100	100
D6	396	gtaatttcagctcgtggggccaaaggggcgctgtcactgtctcgcaggtgtgtgagcggtc	455	1	455	100	0.0	0.0	100	100
Q7	362	cagcgcggaaggtgtgctcgcgcgtgtgcgagatcg---gagttttgtatgcccacaactccac	418	1	418	100	0.0	0.0	100	100
D6	456	cagcgcggaaggtgtgctcgcgcgtgtgcgagatcg---gagttttgtatgcccacaactccac	515	1	515	100	0.0	0.0	100	100
Q7	419	tcaattgtctggttacatcttgagacaacacagcctccatctctctgacaagtcgaagtcagaagcc	478	1	478	100	0.0	0.0	100	100
D6	516	tcaattgtctggttacatcttgagacaacacagcctccatctctctgacaagtcgaagtcagaagcc	575	1	575	100	0.0	0.0	100	100
Q7	479	tcttgcgatgatgatgagaagacatattgaaattggttgtttaacagaagccaaagcagctctc	538	1	538	100	0.0	0.0	100	100
D6	576	tcttgcgatgatgatgagaagacatattgaaattggttgtttaacagaagccaaagcagctctc	635	1	635	100	0.0	0.0	100	100
Q7	539	caaaagcgcccaactcctatctgtctgtcctcaaaacttgagctcctggagctccctcaagagcttcaatg	598	1	598	100	0.0	0.0	100	100
D6	636	caaaagcgcccaactcctatctgtctgtcctcaaaacttgagctcctggagctccctcaagagcttcaatg	695	1	695	100	0.0	0.0	100	100
Q7	599	gcacgtgatcagaagagacagatctcacactgaaatacaacaagaaggtggaagctgagagatttgg	658	1	658	100	0.0	0.0	100	100
D6	696	gcacgtgatcagaagagacagatctcacactgaaatacaacaagaaggtggaagctgagagatttgg	755	1	755	100	0.0	0.0	100	100
Q7	659	gagttattatttctgtgcgaaggtaacacatctccgcgtcaactgttcgtgtctgcccacaagc	718	1	718	100	0.0	0.0	100	100
D6	756	gagttattatttctgtgcgaaggtaacacatctccgcgtcaactgttcgtgtctgcccacaagc	815	1	815	100	0.0	0.0	100	100
Q7	719	tggaatcaaa 729								
D6	816	tggaatcaaa 826								
RESULT	9									
XX	X77245									
XX	X77245	standard; DNA; 753 bp.								
XX	X77245;									
XX	04-AUG-1999	(first entry)								
XX	DE	Mouse scFV fragment 4-7 encoding DNA.								
XX	OS	Mus sp.								
XX	PN	MO925818-A1.								
XX	PD	27-MAY-1999.								
XX	FE	16-NOV-1998.								
XX		98WO-EP07313.								

17-NOV-1997; 97EP-0120096.  
 (KUEFE/) KUEFER P.  
 Borschert K, Kuefer P, Lutterbuese R, Raum T, Zettl F;  
 MPI; 1999-338004/28.  
 P-PSDB; Y17962.  
 Phage display system for identification of binding site domains  
 retaining capacity to bind an epitope  
 Disclosure; Fig 6.8; 152pp; English.  
 The invention relates to a method of identifying binding site domains  
 that retain the capacity of binding to a predetermined epitope when  
 positioned C-terminal of at least one further domain in a recombinant bi-  
 or multivalent polypeptide. The method comprises (a) testing a panel of  
 BSD displayed on the surface of a biological display system as part of a  
 fusion protein for binding to a predetermined epitope, where the fusion  
 protein comprises an additional domain positioned N-terminal of the BSD  
 and an amino acid sequence that mediates anchoring of the fusion protein  
 to the surface of the display system; and (b) identifying a BSD that  
 binds to the predetermined epitope. The method is useful to identify bi-  
 or multivalent polypeptides that comprise antibody binding sites capable  
 of efficiently binding to the corresponding antigen. The polypeptides or  
 antibodies identified by the method are useful therapeutically and  
 diagnostically, for e.g. cancer and autoimmune diseases. scFv antibody  
 fragments that bind independently of their position within bifunctional  
 single-chain fusion proteins can be isolated from combinatorial antibody  
 libraries using the new in vitro method. Sequences x77240-248 represent  
 DNA sequences encoding mouse scFv fragments.  
 Sequence 753 BP; 171 A; 188 C; 215 G; 179 T; 0 other:

Query Match	Similarity	59.3%	Score 432.2	DB 20	Length 753
Best Local	Similarity 75.3%	Pred No. 5.4e-115			
Matches 561	Conservative	0	Mismatches 163	Indels 21	Gaps 1

  

QY	6	gcacgtgcacagctctcgtgagcagagcttcttgagtcagagggccctcaatgccaattgttcctg	65
Db	9	gtcgtccgagcagctgcagctgcagctgcagctgcagctgcagctgcagctgcagctgcagctgc	68
QY	66	ccacagctctgtgcttcaacatcaagaactactatactgcactggtgtgaagcagagcgcttga	125
Db	69	caaggtctcgtggtacacacttcaacaactatgatttaagcgtggtgtgaagcagagcgcttg	128
QY	126	acagggcctcgagatgtagtattgtagtattgtagtattgtagtattgtagtattgtagtattgccc	185
Db	129	acaggtctcttgatgtgattctgtagagagttatcttactctgaatttggtgaattgcttctcaatga	188
QY	186	gaaggtccagggcgaagggccacatctactctgacagacacaccccaatacagctactcgtga	245
Db	189	gaagttcaagggcgaagggccacacactgactgcgagacaaatcccccagcagagctccatgga	248
QY	246	gtctcagcagctctgacatctcgaagaaactgcgctctatattg-----	287
Db	249	gtctcgcagctgactcctcgtgagactctcgtcttacttctctgtgcaagagcgggataccta	308
QY	288	-----taattttacgggagatgctcttggaactattggggccaagagagacacagctcacgcgtc	344
Db	309	cgaatactaactacgactgtaactctgatatgtctctggggccaagagagacacagctcacgcgtc	368
QY	345	ctaagttgagaggggtgtacagcgggaggggtggtcctgcgtgcgtgcgtgcgtgcgtgcgtgc	404
Db	369	ctaaggttgggtgggtgtctcggcgggcgcgcccggtgggtgggtgtgtcttcggagcccgat	428
QY	405	gtacaaatccacactactctgttgtaacacacacacacacacacacacacacacacacacacac	464
Db	429	gtacccagactccactctccctcctgcctgcagctcttggtgagataaagccctccatctcttcag	488
QY	465	gtcaaatctcagagcctcttgtagatgtatgtagaagacacatattgatttgattgtgtatagag	524



Db 489 atctagtcagagcctgtctacacagtaacacacccattacattgttacctgcagaa 548  
 Oy 525 gccaaagcagctcacaagcgccttaattctgtgtctaacgcgactcggagctcc 584  
 Db 549 gccaaagcagctcacaagcgccttaattctgtgtctaacgcgactcggagctcc 608  
 Oy 585 tcaacagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 644  
 Db 609 agacagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 668  
 Oy 645 ggcctgagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 704  
 Db 669 ggcctgagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 728  
 Oy 705 tgcctgagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 729  
 Db 729 aggggagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 753  
  
 RESULT 10  
 ID 090663 standard; DNA; 810 BP.  
 AC 090663;  
 DT 26-JAN-1996 (first entry)  
 DE MFE-23 antibody coding sequence.  
 KM Antibody; MFE-23; carcinoembryonic antigen; CEA; colorectal tumour;  
 KW therapy; diabody; ds.  
 OS Mus musculus.  
 XX  
 XX Key Location/Qualifiers  
 FH misc\_feature 79..438  
 FT /tag= a  
 FT /note= "variable heavy chain"  
 FT misc\_feature 439..483  
 FT /tag= b  
 FT /note= "linker region"  
 FT misc\_feature 484..801  
 FT /tag= c  
 FT /note= "variable light chain"  
 XX  
 PN W09515341-A1.  
 XX  
 PD 08-JUN-1995.  
 XX  
 PF 05-DEC-1994; 94WO-GB02658.  
 XX  
 PR 03-DEC-1993; 93GB-0024807.  
 XX  
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
 XX  
 PI Begent RHJ, Chester KA, Hawkins RE;  
 XX  
 DR WPI; 1995-215234/28.  
 DR P-PSDB; R75719.  
 XX  
 PT Antibody for carcinoembryonic antigen - for treatment and diagnosis  
 of colorectal cancer  
 XX  
 PS Claim 3; Page 48-49; 72pp; English.  
 XX  
 CC This sequence represents the coding sequence for the MFE-23 antibody.  
 CC The encoded protein is an antibody against carcinoembryonic antigen  
 CC (CEA). CEA is a marker antigen for cancer imaging and therapy. The  
 CC MFE-23 antibody sequence was obtained using phage technology. In this  
 CC process, mice were immunised with CEA. The antibody variable region  
 CC genes obtained from these mice were then amplified from cDNA and cloned  
 CC as a single chain Fv (scFv) into bacteriophage vectors, producing a

CC library. The phages that bound to biotinylated CEA were selected and  
 CC amplified, and this sequence (and the protein it encodes) were selected.  
 CC The MFE-23 antibody was found to have good specificity and affinity for  
 CC CEA, meaning that it can be used in targeted anti-tumour therapies. A  
 CC humanised antibody with the complementary determining regions of MFE-23  
 CC may be made by CDR grafting. The antibody may be used for the treatment  
 CC by surgery or therapy of a colorectal tumour, or in the diagnosis of a  
 CC colorectal tumour. MFE-23 may also be used to make diabodies (bivalent  
 CC or bispecific antibody fragments which bind to two different antigens),  
 CC and may be linked to an antitumour agent or a detectable label.  
 XX  
 SQ Sequence 810 BP; 189 A; 220 C; 222 G; 179 T; 0 other;  
  
 Query Match 59.3%; Score 432.2; DB 16; Length 810;  
 Best Local Similarity 76.7%; Pred. No. 5.5e-115;  
 Matches 568; Conservative 0; Mismatches 143; Indels 30; Gaps 2;  
  
 Oy 1 caggtcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 60  
 Db 79 caggtcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 138  
 Oy 61 tctctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 120  
 Db 139 tctctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 198  
 Oy 121 cctgacagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 180  
 Db 199 cctgacagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 258  
 Oy 181 gccccgaagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 240  
 Db 259 gccccgaagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 318  
 Oy 241 ctgcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 291  
 Db 319 ctgcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 378  
 Oy 222 ---tttaagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 348  
 Db 379 cagctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 438  
 Oy 349 ggtgagctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 408  
 Db 439 ggtgagctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 498  
 Oy 409 caactcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 468  
 Db 499 cagctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 558  
 Oy 469 agtcaagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 528  
 Db 559 agtcaagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 600  
 Oy 529 gccagctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 588  
 Db 601 gccagctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 660  
 Oy 589 aggtcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 648  
 Db 661 cgttcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 720  
 Oy 649 gaggtcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 708  
 Db 721 gaggtcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 780  
 Oy 709 gccacacagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 729  
 Db 781 gccacacagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 801  
  
 RESULT 11  
 288358

ID 288358 standard; DNA; 1637 BP.  
XX  
AC 288358;  
XX  
DT 04-MAY-2000 (first entry)  
XX  
DE Bispecific anti-zeta-chain/anti-EpCAM antibody nucleotide sequence.  
XX  
KW Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;  
KW complementary region; CDR; autoimmune disease; cytotoxic;  
KW immune deficiency; T-cell malignancy; infectious disease; antiviral;  
KW immunosuppressive; antimicrobial; immune response modulator; NK-cell; ds.  
XX  
OS Rattus norvegicus.  
OS Synthetic.  
XX  
PN MO200003016-A1.  
XX  
PD 20-JAN-2000.  
XX  
PE 09-JUL-1999; 99WO-EP04838.  
XX  
PR 10-JUL-1998; 98EP-0112867.  
XX  
PA (CONN-) CONNEX GMBH.  
XX  
PI Relter C;  
XX  
DR WPI: 2000-160926/14.  
DR P-PSDB: Y178328.  
XX  
PT New oligonucleotide, polypeptide, antibody useful for treating  
XX autoimmune disease, immune deficiencies, T-cell malignancies and  
XX infectious diseases -  
XX  
PS Example 9; Page 74; 79pp; English.  
XX  
CC The present invention describes a nucleic acid molecule (I) encoding at  
CC least one complementary determining region (CDR) of a variable region of  
CC an antibody which specifically interacts with the extracellular domain of  
CC the human zeta-chain. The antibody whose CDR of a variable region is  
CC encoded by (I), is obtained by immunising a rat with jurkat cells and  
CC subsequently with a conjugate comprising a carrier molecule and a  
CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The  
CC anti-zeta-chain antibody is useful for the treatment and prevention of  
CC autoimmune diseases, immune deficiencies, T-cell malignancies,  
CC infectious diseases and the suppression of immune response preferably in  
CC order to avoid graft rejection after organ transplantation, malignancies,  
CC or viral infections. The antibody, and fragments of it, can be useful for  
CC the enhancement or suppression of NK-cell dependent immunity or for the  
CC treatment of NK-cell derived malignancies. It can also be useful for the  
CC determination of zeta-chain or eta-chain expression on NK-cells,  
CC T-lymphocytes or their precursors. The present sequence encodes a  
CC bispecific anti-zeta-chain/anti-EpCAM antibody, from an example from  
CC the present invention.  
XX  
SQ Sequence 1637 BP; 398 A; 404 C; 436 G; 399 T; 0 other;

Query Match 59.3%; Score 437.2; DB 21; Length 1637;  
Best Local Similarity 75.3%; Pred. No. 7,1e-115;  
Matches 561; Conservative 0; Mismatches 163; Indels 21; Gaps 1;

QY 6 gcaagctcagcagctcgtggtgagctggtgagctcagggcctcagtgacgttcctg 65  
II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII  
DB 825 gctgctgcagcagctcgtggtcgtgagctcgtggtcgtggtcgtggtcgtg 884  
II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII  
QY 66 cacagcttcgtgctcacaataaagactatactatgacactgggtgaagcagagctga 125  
II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII  
DB 885 caagcttcgtgctcacaactcacaactatgtttaagctgggtgaagcagagctgg 944  
II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII  
QY 126 acaaggcctcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtg 185  
II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII

DB 945 acaagctccttggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1004  
QY 186 gaagttccagggcagagggcaccatagctgacagacacatccctccatagccttactgca 245  
II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII  
DB 1005 gaagttccagggcagagggcaccatagctgacagacacatccctccatagccttactgca 1064  
QY 246 gctcagcagcctggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 287  
II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII  
DB 1065 gctcagcagcctggtggtggtggtggtggtggtggtggtggtggtggtggtggtg 1124  
QY 288 ----tatcttaccgggagagcttggtggtggtggtggtggtggtggtggtggtggtggtggtggtg 344  
II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII  
DB 1125 cgatactaacctcagcagctggtggtggtggtggtggtggtggtggtggtggtggtggtg 1184  
QY 345 ctcaagtgagggcgtggtcagggcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 404  
II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII  
DB 1185 ctcaagtgagggcgtggtcagggcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1244  
QY 405 gacccaaactcactcacttctggttaccattggtggtggtggtggtggtggtggtggtggtggtggtggtggtg 464  
II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII  
DB 1245 gacccaaactcactcacttctggttaccattggtggtggtggtggtggtggtggtggtggtggtggtggtggtg 1304  
QY 465 gtcaagtcagagcctccttggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 524  
II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII  
DB 1305 atctagtcagagcctccttggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1364  
QY 525 gccagggcagctcctcagagcgtcctatctatctggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 584  
II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII  
DB 1365 gccagggcagctcctcagagcgtcctatctatctggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1424  
QY 585 tgacaggtcactggtcaggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 644  
II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII  
DB 1425 agacaggtcaggtggtcaggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1484  
QY 645 ggtcagaggtg 704  
II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII  
DB 1485 ggtcagaggtg 1544  
QY 705 tgctgacacccagcctggaatcaaa 729  
II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII  
DB 1545 aggggggacacagcttgatcaaa 1569

RESULT 12  
X77241  
ID X77241 standard; DNA; 753 BP.  
XX  
AC X77241;  
XX  
DT 04-AUG-1999 (first entry)  
XX  
DE Mouse scFv fragment 3-5 encoding DNA.  
XX  
KW Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;  
KW autoimmune disease; scFv-antibody; single-chain Fv; mouse; ss.  
XX  
OS Mus sp.  
XX  
PN MO9925818-A1.  
XX  
PD 27-MAY-1999.  
XX  
PE 16-NOV-1998; 98WO-EP07313.  
XX  
PR 17-NOV-1997; 97EP-0120096.  
XX  
PA (KUFE/) KUFE P.  
XX  
PI Borschert K, Kufer P, Lutterbuese R, Raum T, Zetl F;  
XX  
DR WPI: 1999-338004/28.  
DR P-PSDB: Y17958.  
XX





OY	476	gcccttcgtgtagtgatgaagaacatttggattggtgtgttaagaggccagcgaagt	535
Db	1326	gtgtca-----agttacaatgcactgttccagaagaagccaggaact	1367
OY	536	ctccaagaagcccatatcatctgtgtctcaaacctggacctgaaatccctacaagttca	595
Db	1368	ctccaacactctgatttatagacaatccaacctcgcttcttgaaatccctctcgtctta	1427
OY	596	ctggcagctgatcagcagagatttcaacactgnaaatcaacagagtggaagctgaagtt	655
Db	1428	gtggcagctgatcctggaaccttactctctccaatacagccgaatgagagctgaagt	1487
OY	656	tggsgagtttatattgtgtgcaagagfacacatcttcgcgtaccgtgtgtctgacaca	715
Db	1488	ctgcacctatcatctgcccaacagagatgattaccacctcagttcgtgtctgacacca	1547
OY	716	agctcgaaatcaaa 729	
Db	1548	agctgagctgaaaa 1561	
RESULT	15		
X86942			
ID	X86942	strand: DNA; 726 BP.	
AC	X86942;		
XX			
DT	24-SEP-1999	(first entry)	
DE	Antibody BIOC7 encoding DNA.		
XX			
KW	Prostate-specific antigen; PSA; anti-chymotrypsin; ACT; antibody;		
KM	diagnostic assay; PSA-ACT; prostate cancer; tumour; immunotherapy;		
KW	BIOC7, ds.		
XX			
OS	Homo sapiens.		
XX			
PN	EP934953-A2.		
XX			
PD	11-AUG-1999.		
XX			
PF	01-DEC-1998; 98EP-0122546.		
PR	03-DEC-1997; 97US-0067428.		
XX			
PA	(BOE ) BOEHRINGER MANNHEIM CORP.		
PI	Mahoney W, Sawyer JR, Winter GP;		
DR	WI; 1999-432068/37.		
DR	P-PSDB; Y21884.		
PT	New anti-complex antibody useful for diagnosing prostate cancer		
PS	Disclosure; Page 28-30; 42pp: English.		
XX			
CC	The invention relates to an antibody that binds a complex between		
CC	prostate-specific antigen (PSA) and anti-chymotrypsin (ACT), and has an		
CC	affinity for the complex which is at least 10 fold higher than the		
CC	affinity for either PSA or ACT alone. The antibody is used in diagnostic		
CC	assays to detect PSA-ACT in serum samples from patients. The levels of		
CC	PSA-ACT complex increase in patients suffering from prostate cancer		
CC	compared to the levels in patients with benign or no growths in the		
CC	prostate. Therefore detection of PSA in complex with ACT is useful for		
CC	the early detection of prostate tumours, by distinguishing between benign		
CC	and malignant conditions of the prostate as well as for the management of		
CC	patients with prostate cancer, such as the disclosure of metastasis and		
CC	the monitoring of the PSA levels after treatment. The antibodies may		
CC	also be used in immunotherapy, affinity chromatography and isolation or		
CC	purification of PSA-ACT. Unlike prior art antibodies which bind to		
CC	PSA-ACT complexes but may also bind PSA or ACT alone, the present		
CC	antibody is specific for PSA-ACT alone. Diagnostic assays using the		
CC	antibodies are more accurate in diagnosing prostate cancer as they only		

CC detect the intact complex of PSA-Act. Sequences Y21880-884 represent  
 CC specific examples of antibodies directed against PSA-Act. The present  
 CC sequence represents the nucleotide sequence of antibody B10C7.  
 XX  
 SQ Sequence 726 BP; 167 A; 178 C; 217 G; 161 T; 3 other;

SQ Sequence 726 BP; 167 A; 178 C; 217 G; 161 T; 3 other;

Query Match	57.3%;	Score 418;	DB 20;	Length 726;
Best Local Similarity	75.3%;	Pred. No. 6.4e-11;		
Matches 549;	Conservative 1;	Mismatches 167;	Indels 12;	Gaps 2

OY	1	caagtcgcagcgcagcagctctctgggcagagacctctgtgaggtccaaaggccctccagtcacattg	60
Db	7	caagtcgcagcgcagcagctctctgggcagagacctctgtgaggtccaaaggccctccagtcacattg	66
OY	61	tccgcgacaagctctctggctccaacattaaagactacatactgacacgcgggtcgaaagcgaag	120
Db	67	tccgcgacaagctctctggctccaacattaaagactacatactgacacgcgggtcgaaagcgaag	126
OY	121	ccctgacaagggcctcgsgctgagatctgagatctgacatctgagatacgtgtgatactgacat	180
Db	127	ccctgacaagggcctcgsgctgagatctgagatctgacatctgagatacgtgtgatactgacat	186
OY	181	gcccgcgaagctccagggccaaaggccacatctgacgcagacacacccccaataaagcttc	240
Db	187	tcaagaagaagctccagggccaaagtcacatctacccaagagacacaccccgccagacacgtcc	246
OY	241	ctgcagctcacaicacaacccggcgcctcgtgaagacacgcgcgtctcatctgttaatttcagg	300
Db	247	atggaagctcgacagcccggaatctctgaaagaaacggccggtgtattacggt-----gca	297
OY	301	gatcgcttgagctatctgtggggccaaaggagacacagctccacgtctctccaaagctggagcggt	360
Db	298	agaaggaatcgctttctggggccaaaggtacccctgctcacgctccmagtctgtggagcggt	357
OY	351	tcaagccgagatctgctctgctgcggtgtgcgagtcagatcttgatggacccaactcaccc	420
Db	358	tcaagccgagatctgctctgctgcggtgtgcgagtcagatcttgatggatggacccaactcaccc	417
OY	421	actctgtcgtgtacacattctggacaacacacgcgtccatctctctggaagcacaagtcagagccc	480
Db	418	tctctgttcggtccaacccctggacaagccgctccatctctctgcaagctgagtcagaacccc	477
OY	481	ttagaatagtctggaagaacatatcttgaattggttgatcaagagccaaagccaggtctcca	540
Db	478	ctgcaatagtctggaagaacatatcttgaattggttgatcaagagccaaagccaggtctcca	537
OY	541	aagcgcctaactctatctcgtggtctaaactcgtgacactcggagctccctcaacaggtctacgtgc	600
Db	538	cagctccctgacactctgaagattctccaacccggtctctctgagtgccaagatggttcaagtgc	597
OY	601	agtgatcagaaggaagaattccaacgtcaaaatacaacagagctggaagctgaagattggga	660
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OY	661	gttattattctcggcgaaggtacacatctccgcgtcacggtctggtctgtcgccacaagacgcg	720
Db	658	gttattattctcggcgaaggtacacatctccgcgtcacggtctggtctgtcgccacaagacgcg	714
OY	721	gaaatcaaa 729	
Db	715	gaaatcaaa 723	

Search completed: February 17, 2001, 23:01:10  
Job time: 16451 sec ;

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2001, 20:27:22 ; Search time 2148.34 Seconds

(without alignments)  
1473.291 Million cell updates/sec

Title: US-09-297-181-1

Perfect score: 729  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 12370408 seqs, 2170871038 residues

Total number of hits satisfying chosen parameters: 24740816

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_NA.\*

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3: /cgn2\_6/ptodata/2/pna/US07\_COMB.seq.\*  
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19: /cgn2\_6/ptodata/2/pna/US095\_COMB.seq.\*  
20: /cgn2\_6/ptodata/2/pna/US095A\_COMB.seq.\*  
21: /cgn2\_6/ptodata/2/pna/US095B\_COMB.seq.\*  
22: /cgn2\_6/ptodata/2/pna/US095C\_COMB.seq.\*  
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27: /cgn2\_6/ptodata/2/pna/US099\_COMB.seq.\*  
28: /cgn2\_6/ptodata/2/pna/US100\_COMB.seq.\*  
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37: /cgn2\_6/ptodata/2/pna/US109\_COMB.seq.\*  
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43: /cgn2\_6/ptodata/2/pna/US115\_COMB.seq.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	729	100.0	729	16	US-09-297-181-1 Sequence 1, Appl
2	717.8	98.5	768	13	US-08-930-480-4 Sequence 4, Appl
3	717.8	98.5	768	13	US-08-930-480-4 Sequence 4, Appl
4	716.2	98.2	749	13	US-08-983-035-16 Sequence 46, Appl
5	716.2	98.2	1611	13	US-08-983-035-16 Sequence 37, Appl
6	505	69.3	1135	16	US-09-203-958-2 Sequence 2, Appl
7	464.8	63.8	819	55	US-09-523-095A-33 Sequence 3, Appl
8	464.8	63.8	828	55	US-09-523-095A-31 Sequence 31, Appl
9	460.8	63.2	747	16	US-09-297-181-3 Sequence 39, Appl
10	460	63.1	741	55	US-09-523-095A-39 Sequence 29, Appl
11	458.4	62.9	819	55	US-09-523-095A-29 Sequence 25, Appl
12	458.4	62.9	828	55	US-09-523-095A-25 Sequence 30, Appl
13	438	60.1	714	21	US-09-559-019-50 Sequence 29, Appl
14	436.4	59.9	720	21	US-09-559-019-50 Sequence 16, Appl
15	426.6	58.5	753	1	PCR-US00-19843-16 Sequence 9, Appl
16	426.6	58.5	792	1	PCR-US00-19843-9 Sequence 15, Appl
17	425.2	58.3	1679	17	US-09-364-088-15 Sequence 15, Appl
18	425.2	58.3	1679	19	US-09-523-279-15 Sequence 15, Appl
19	425.2	58.3	1679	55	US-09-188-082-15 Sequence 13, Appl
20	418	57.3	726	16	US-09-202-000-13 Sequence 15, Appl
21	418	57.3	726	16	US-09-202-000-15 Sequence 31, Appl
22	409.4	56.2	830	17	US-09-358-371A-31 Sequence 22, Appl
23	405.8	55.7	879	16	US-09-235-073-22 Sequence 17, Appl
24	402.6	55.2	786	1	PCR-US00-19843-17 Sequence 10, Appl
25	402.6	55.2	792	1	PCR-US00-19843-10 Sequence 35, Appl
26	392	53.8	1047	22	US-09-646-028-35 Sequence 37, Appl
27	392	53.8	1086	22	US-09-646-028-37 Sequence 36, Appl
28	369.6	50.7	783	21	US-09-589-870-36 Sequence 33, Appl
29	361.8	49.6	772	7	US-08-331-396-33 Sequence 33, Appl
30	361.8	49.6	772	7	US-08-331-396A-33 Sequence 33, Appl
31	361.8	49.6	772	7	US-08-331-396C-33 Sequence 33, Appl
32	361.8	49.6	772	7	US-08-331-396D-33 Sequence 33, Appl
33	361.8	49.6	772	7	US-08-331-397-33 Sequence 33, Appl
34	361.8	49.5	772	7	US-08-331-398-33 Sequence 33, Appl
35	361.8	49.5	772	11	US-08-759-804-33 Sequence 33, Appl
36	361.8	49.6	772	16	US-09-227-653-33 Sequence 1, Appl
37	358.2	49.1	771	19	US-09-526-728-1 Sequence 57, Appl
38	358.2	49.1	780	19	US-09-526-728-1 Sequence 59, Appl
39	356.8	48.3	1725	18	US-09-468-029-57 Sequence 31, Appl
40	352.4	48.3	720	16	US-09-266-595-7 Sequence 31, Appl
41	349.2	47.3	1668	18	US-09-468-029-59 Sequence 31, Appl
42	349	47.9	738	7	US-08-331-396C-31 Sequence 31, Appl
43	349	47.9	738	7	US-08-331-396D-31 Sequence 31, Appl
44	349	47.3	741	7	US-08-331-396-31 Sequence 31, Appl
45	349	47.3	741	7	US-08-331-396A-31 Sequence 31, Appl

#### ALIGNMENTS

RESULT 1  
US-09-297-181-1  
Sequence 1, Application US/09297181  
GENERAL INFORMATION:  
APPLICANT: Bracco, Laurent  
APPLICANT: Debussche, Laurent  
TITLE OF INVENTION: ANTI-P53 SINGLE-CHAIN ANTIBODY FRAGMENTS AND THEIR USES  
FILE REFERENCE: ST96030-US  
CURRENT APPLICATION NUMBER: US/09/297,181  
CURRENT FILING DATE: 1999-04-26  
EARLIER APPLICATION NUMBER: PCT/FR97/01921  
EARLIER FILING DATE: 1997-10-27  
EARLIER APPLICATION NUMBER: FR96/13176  
EARLIER FILING DATE: 1996-10-29  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 729  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(729)  
US-09-297-181-1

Query Match 100.0%; Score 729; DB 16; Length 729;  
Best Local Similarity 100.0%; Pred. No. 1.8e-207;  
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 caggttcagctgcagcagctctggtgagcagagctgtgaggtcagggcctcagtaagt 60  
QY 61 tccgcagcagcttcgcttcacattaaagacacacatgtcagctgggtgaagcagag 120  
DB 61 tccgcagcagcttcgcttcacattaaagacacacatgtcagctgggtgaagcagag 120  
QY 121 cctgaacagagcctgagatgagatgagatgagatgagatgagatgagatgagat 180  
DB 121 cctgaacagagcctgagatgagatgagatgagatgagatgagatgagatgagat 180  
QY 181 gccgcagagctcagagcagagcagacacacacacacacacacacacacacacac 240  
DB 181 gccgcagagctcagagcagagcagacacacacacacacacacacacacacacac 240  
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QY 301 gatgcttgcagctatgagcagcagcagcagcagcagcagcagcagcagcagcagc 360  
DB 301 gatgcttgcagctatgagcagcagcagcagcagcagcagcagcagcagcagcagc 360  
QY 361 tcagcagcagagctgctgctgctgctgctgctgctgctgctgctgctgctgctg 420  
DB 361 tcagcagcagagctgctgctgctgctgctgctgctgctgctgctgctgctgctg 420  
QY 421 acttttcggttaccattgagcagcagcagcagcagcagcagcagcagcagcagcagc 480  
DB 421 acttttcggttaccattgagcagcagcagcagcagcagcagcagcagcagcagcagc 480  
QY 481 ttgagatgagtgagaaagacatattgagtggtttgagagagcagagcagcagcagc 540  
DB 481 ttgagatgagtgagaaagacatattgagtggtttgagagagcagagcagcagcagc 540  
QY 541 aagcgcctaatctatctgtgtctaaactgagcagcagcagcagcagcagcagcagc 600  
DB 541 aagcgcctaatctatctgtgtctaaactgagcagcagcagcagcagcagcagcagc 600  
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DB 601 agtgcagcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 660

QY 661 gttattattctgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 720  
DB 661 gttattattctgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 720  
QY 721 gaattcaaa 729  
DB 721 gaattcaaa 729

RESULT 2  
US-08-930-480-4  
Sequence 4, Application US/08930480  
GENERAL INFORMATION:  
APPLICANT: BRACCO, Laurent  
APPLICANT: SCHMEIGHOFER, Fablen  
APPLICANT: TOCQUE, Bruno  
TITLE OF INVENTION: CONDITIONAL EXPRESSION SYSTEM  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Road, Malistop 3043  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/930,480  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/03841  
FILING DATE: 31-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/FR96/00477  
FILING DATE: 29-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Fehner Esq., Paul F.  
REGISTRATION NUMBER: 35,135  
REFERENCE/DOCKET NUMBER: ST95021-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3839  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 768 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-930-480-4

Query Match 98.5%; Score 717.8; DB 13; Length 768;  
Best Local Similarity 99.0%; Pred. No. 4.2e-204;  
Matches 722; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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DB 28 CAGGTTCAGCTGCAGCAGCTGTGGCGCAGAGCTGTAAAGTCAGAGGCGCTCAGTCAAGT 87  
QY 61 tccgtcagcagctctgcttcacattaaagacacacacacacacacacacacacacac 120  
DB 88 TCGTGCAGAGCTTCTGGCTTCAACATTAAGACTATATGACACTGGGTGAAGCAGAG 147  
QY 121 ccggaacagagcctgag 180  
DB 148 CCGGAACAGGCGCTGAGAGTGGATTGATGATCTTAAGATGATGATGATGATGATGAT 207



Oy	181	gccccgaagcttcacagggcaagggccacatctgacatgcacacacatctctcaataagagcttac	240
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Oy	241	ctgcagctcagcagccttgacatctgtagacactgcgcgtctattatctgtaatttttacgag	300
Db	268	ctgcagctcagcagccttgacatctgtagacactgcgcgtctattatctgtaatttttacgag	327
Oy	301	gatgcttgtagactatctggcgcaagggagacccagtcacgcgtctcctctaagtgtgagggcgt	360
Db	328	gatgcttgtagactatctggcgcgcaagggagacccagtcacgcgtctcctctaagtgtgagggcgt	387
Oy	361	tcagcgcgagaggtgycgtctcgcgctggtgycgagatcggatgttttbgatgacccaactcaccac	420
Db	388	tcagcgcgagaggtgycgtctcgcgctggtgycgagatcggatgttttbgatgacccaactcaccac	447
Oy	421	acttgctgcgtttaccatttgagcaaacacagcctccatctctctgcaagtcaagtcagagctc	480
Db	448	acttgctgcgtttaccatttgagcaaacacagcctccatctctctgcaagtcaagtcagagctc	507
Oy	481	ttgagatagtagtgagaaagacatatttgaaattggtgtttacagagcgcaagcgcaagtcaca	540
Db	508	ttgagatagtagtgagaaagacatatttgaaattggtgtttacagagcgcaagcgcaagtcaca	567
Oy	541	aagcgcccaatctatctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg	600
Db	568	aagcgcccaatctatctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg	627
Oy	601	agtgatgaaggagacagatttacaactgaaatacaacagagtagggagctgtgagattggga	660
Db	628	agtgatgaaggagacagatttacaactgaaatacaacagagtagggagctgtgagattggga	687
Oy	661	gttatatctgctgcaaggtacacatctccgcctcagcttgcgctgctgctgctgctgctgctgctg	720
Db	688	gttatatctgctgcaaggtacacatctccgcctcagcttgcgctgctgctgctgctgctgctgctg	747
Oy	721	gaatcctaaa	729
Db	748	gaattttaa	756
<p>RESULT 3</p> <p>US-08-930-480A-4</p> <p>Sequence 4, Application US/08930480A</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: BRACCO, Laurent</p> <p>APPLICANT: SCHWEIGHOFFER, Fabien</p> <p>APPLICANT: TOCOUE, Bruno</p> <p>TITLE OF INVENTION: CONDITIONAL EXPRESSION SYSTEM</p> <p>FILE REFERENCE: ST95021-US</p> <p>CURRENT APPLICATION NUMBER: US/08/930.480A</p> <p>CURRENT FILING DATE: 1998-01-21</p> <p>PRIOR APPLICATION NUMBER: PCT/FR96/00477</p> <p>PRIOR FILING DATE: 1996-03-29</p> <p>PRIOR APPLICATION NUMBER: FR95/03841</p> <p>PRIOR FILING DATE: 1995-03-31</p> <p>NUMBER OF SEQ ID NOS: 32</p> <p>SOFTWARE: PatentIn Ver. 2.1</p> <p>SEQ ID NO 4</p> <p>LENGTH: 768</p> <p>TYPE: DNA</p> <p>ORGANISM: Artificial Sequence</p> <p>FEATURE:</p> <p>OTHER INFORMATION: Description of Artificial Sequence: ScFv Against</p> <p>US-08-930-480A-4</p>			

Query Match	98.5%;	Score 717.8;	DB 13;	Length 768;
Best Local Similarity	99.0%;	Pred. No. 4.2e-204;		
Matches 722;	Conservative	0;	Mismatches 7;	Indels 0;
				Gaps 0;

QY	1	caagrgcagcgcgcagcagcaatctcgggggcagaaagcttctggaggtcaaggggccctcaagctcaaatgtg	60
DB	28	caagrgcagcgcgcgcagcagcaatctcgggggcagaaagcttctggaggtcaaggggccctcaagctcaaatgtg	87
QY	61	tcctctgcaaaagcttctctggtcttcaaatlaaagaactactactatactgacactgtgtgaagcagaag	120
DB	88	tcctctgcaaaagcttctctggtcttcaaatlaaagaactactactatactgacactgtgtgaagcagaag	147
QY	121	ccctgaacaagggccctgagagctgagattgagatgtatctctgagaatgtgtgatactgaaat	180
DB	148	ccctgaacaagggccctgagagctgagattgagatgtatctctgagaatgtgtgatactgaaat	207
QY	181	ggcccccgaaggtcttccaaaggagggccacactctgactctgcagacaatactctccaataacagcctac	240
DB	208	ggcccccgaaggtcttccaaaggagggccacactctgactctgcagacaatactctccaataacagcctac	265
QY	241	ctgcagaccccaagcagcctctgacactctgaaagacaactctccgtctctactttgtlaatttttaagg	300
DB	268	ctgcagaccccaagcagcctctgacactctgaaagacaactctccgtctctactttgtlaatttttaagg	327
QY	301	gattgctttggacattatgtggggcccaaggaggaaccaaggttcaacgctctcctaagtgtgagggcgt	360
DB	328	gattgctttggacattatgtggggcccaaggaggaaccaaggttcaacgctctcctaagtgtgagggcgt	387
QY	361	tcaaggccggagagttggtctctcggcggtggcgagatccgagatgttttgatgacccaacacccacatc	420
DB	388	tcaaggccggagagttggtctctcggcggtggcgagatccgagatgttttgatgacccaacacccacatc	447
QY	421	actttgctggtttacaacatttgacaacaccaagcctccactctcttccaaagtcagaatcagaagcttc	480
DB	448	actttgctggtttacaacatttgacaacaccaagcctccactctcttccaaagtcagaatcagaagcttc	507
QY	481	ttggaatagttgagtaagaagacatatgtgaattgtgttacaagagccagggccagcttcca	540
DB	508	ttggaatagttgagtaagaagacatatgtgaattgtgttacaagagccagggccagcttcca	567
QY	541	aagggccccaactctatctgtgtcttaaaatggaaacctctgagagccctctgacaagtttacaatggc	600
DB	568	aagggccccaactctatctgtgtcttaaaatggaaacctctgagagccctctgacaagtttacaatggc	627
QY	601	agtgtgatacagggacagatattcacactgaaataacaaacagagtgtagagggctctgagatttggga	660
DB	628	agtgtgatacagggacagatattcacactgaaataacaaacagagtgtagagggctctgagatttggga	687
QY	661	gttatattctctggtggaaggtacaacatctctcgctcaagttcgggtcgtggtgacccaagctg	720
DB	688	gttatattctctggtggaaggtacaacatctctcgctcaagttcgggtcgtggtgacccaagctg	747
QY	721	gaatatcaaa 729	
DB	748	gaatatcaaa 756	

RESULT 4  
US-08-983-035-46  
: Sequence 46, Application US/08983035  
: GENERAL INFORMATION:  
: APPLICANT: BRACCO, Latent  
: APPLICANT: CONSELLER, Emmanuel  
: TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL  
: TITLE OF INVENTION: US\$ THEROF  
: NUMBER OF SEQUENCES: 59  
: CORRESPONDENCE ADDRESS:  
: ADDRESS: Rhone-Poulenc Rorer Inc.  
: STREET: 500 Arcola Road, Mailstop 3C43  
: CITY: Collegeville  
: STATE: PA  
: COUNTRY: USA  
: ZIP: 19426  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS

```

COMPUTER READABLE FORM:
- MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```



Query Match	69.3%	Score 505;	DB 16;	Length 1135;
Best Local Similarity	81.2%;	Pred. No. 3.1e-140;		
Matches 608; Conservative	0;	Mismatches 120;	Indels 21;	Gaps 1

RESULT 7  
 US-09-523-095A-33  
 : Sequence 33. Application US/09523095A  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: FUKUSHIMA, Naoshi  
 :  
 : APPLICANT: UNO, Shinsuke  
 :  
 : APPLICANT: OH-EDA, Masayoshi  
 :  
 : APPLICANT: KIKUCHI, Yasufumi  
 :  
 : TITLE OF INVENTION: APOPTOSIS-INDUCING SINGLE-CHAIN F  
 :  
 : FILE REFERENCE: 065678/0102  
 :  
 : CURRENT APPLICATION NUMBER: US/09/523, 095A  
 :  
 : CURRENT FILING DATE: 2000-03-10  
 :  
 : PRIOR APPLICATION NUMBER: JP 11-63557  
 :  
 : PRIOR FILING DATE: 1999-03-10  
 :  
 : NUMBER OF SEQ ID NOS: 40  
 :  
 : SOFTWARE: PatentIn Ver. 2.1  
 :  
 : SEQ ID NO 33  
 :  
 : LENGTH: 819\*  
 :  
 : TYPE: DNA



Query Match	63.28;	Score 460.8;	DB 16;	Length 747;	.
Best Local Similarity	79.28;	Pred. No. 4.6e-127;			
Matches 594;	Conservative	0;	Mismatches 132;	Indels 24;	Gaps 3

Accession	Sequence	Position
Db	gtccctgatcgcttcacacagagcagcgcgtcctggacagattcaactctccaccatcagcagtt	660
Qy	gtgaaagcctaagaggttggggaggttatattgtcgggaaggtacaaattccgcgtcag	659
Db	gtgcgaagctcgaagacactgcgcgattactattactcaagcaaaa--cttataatctcagcag	717
Qy	ttcggctcctggaccacaaagctggaattcaaa	729
Db	ttcggcggggcaccacaaagcttggaaattcaaa	747

Query Match	63.1%;	Score 460;	DB 55;	Length 741;
Best Local Similarity	77.7%;	Pred. No. 8e-127;		
Matches 569;	Conservative	0;	Mismatches 160;	Indels 3; Gaps 1;

[illegible]



```
QY 181 gccccgaagttccagagcagcgaactatgactgacagacacatccctccatacagcctac 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 247 aatgagaagtccaagggcagagccacacgactgactagagaataccctccagcagcctac 306
QY 241 ctgcagctcagcagcctggtgactgagagacacgctgcctctattatgtaatttttcg- 239
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 307 atggaactcagcagcctggtcctgagactgctgctactactactgtaagaagggtt 366
QY 300 - -gagatcttgagctattgagggcagagcagcagcagcagcagcagcagcagcagc 357
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 367 tactaatgtaacgacgactggtggcagagcagcagcagcagcagcagcagcagcagcagc 426
QY 358 ggttcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 417
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 427 ggttcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 486
QY 418 ctcaacttgcgttccatcagcagcagcagcagcagcagcagcagcagcagcagcagc 477
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 487 ctctccctgcgttgcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 546
QY 478 ctcttgatagtgatgaaagacatattgattggttttaagaggccagcagcagcagc 537
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 547 ctcttcacagtaagaaacacacttcttcaatggttaccataagaagccagcagcagc 606
QY 538 ccaagcgccttaactatctgtgtctaaactgagcagcagcagcagcagcagcagcagc 597
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 607 ccaagcgccttgcctcaacaaagtctcaacagcttcttggtggtccagagcagcagc 666
QY 598 ggcagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 657
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 667 ggcagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 726
QY 658 ggcagcttattatgctgagcagcagcagcagcagcagcagcagcagcagcagcagc 717
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 727 ggcagcttattatgctgagcagcagcagcagcagcagcagcagcagcagcagcagc 786
QY 718 ctggaatacaaa 729
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 787 ctggaatacaaa 798
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
US-09-559-019-30
; Sequence 30, Application US/09559019
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Wille, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: Sequence Listings 1-34 for 381-71
; CURRENT APPLICATION NUMBER: US/09/559,019
; CURRENT FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 714
; TYPE: DNA
; ORGANISM: Mouse
US-09-559-019-30
```

```
Query Match          60.1%; Score 438; DB 21; Length 714;
Best Local Similarity 77.3%; Pred. No. 3,1e-120;
Matches 566; Conservative 0; Mismatches 145; Indels 21; Gaps 2;
```

```
Db 121 cctggaacagggcgtgagtgatgattgattccggaatggttattctgattat 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 gccccgaagttccagagcagcgaactatgactgacagacacatccctccatacagcctac 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 gccccgaagttccagagcagcgaactatgactgacagacacatccctccatacagcctac 240
QY 241 ctgcagctcagcagcctggtgactgagagacacgctgcctctattatgtaatttttcg- 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 ctgcagctcagcagcctggtgactgagagacacgctgcctctattatgtaatttttcg- 300
QY 301 gatgctttgga- -ctatggtggccaaggagcagcagcagcagcagcagcagcagcagc 357
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 ggtgactacgaaggcctacggtggccaaggagcagcagcagcagcagcagcagcagcagc 360
QY 358 ggttcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 417
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 ggttcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420
QY 418 ctcaacttgcgttccatcagcagcagcagcagcagcagcagcagcagcagcagcagc 477
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 gcaatcagctgctgcatctccagagggagagcagcagcagcagcagcagcagcagcagc 480
QY 478 ctcttgatagtgatgaaagacatattgattggttttaagaggccagcagcagcagc 537
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 481 gta- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 522
QY 538 ccaagcgccttaactatctgtgtctaaactgagcagcagcagcagcagcagcagcagc 597
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 523 ccaaacctctgatttgaacacatccacacgctgctctgagcagcagcagcagcagc 582
QY 598 ggcagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 657
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 583 ggcagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 642
QY 658 ggcagcttattatgctgagcagcagcagcagcagcagcagcagcagcagcagcagc 717
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 643 ggcagcttattatgctgagcagcagcagcagcagcagcagcagcagcagcagcagc 702
QY 718 ctggaatacaaa 729
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 703 ctggaatacaaa 714
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-09-559-019-29
; Sequence 29, Application US/09559019
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Wille, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: Sequence Listings 1-34 for 381-71
; CURRENT APPLICATION NUMBER: US/09/559,019
; CURRENT FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Mouse
US-09-559-019-29
```

```
Query Match          59.9%; Score 436.4; DB 21; Length 720;
Best Local Similarity 77.2%; Pred. No. 9,3e-120;
Matches 565; Conservative 0; Mismatches 146; Indels 21; Gaps 2;
```

```

Db      61  tccctgacaaactctgcttcaacaatlaaagaacttctatatgacatggtgtaagcagaag 120
QY      121  cctgaacagagcctgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 180
Db      121  cctgaacagagcctgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 180
QY      181  gccccgaagttcagagcagaagcgaactatgactgacagacatctccctcaataagacctac 240
Db      181  gccccgaagttcagagcagaagcgaactatgactgacagacatctccctcaataagacctac 240
QY      241  ctgacagctcagcagcctgagatctgagagacacgctcccttattatgtaatttttaagg 300
Db      241  ctgacagctcagcagcctgagatctgagagacacgctcccttattatgtaatttttaagg 300
QY      301  gacgcttga---ctatgggccaagggacacagcctccctccctcaagtgagagc 357
Db      301  gacgcttga---ctatgggccaagggacacagcctccctccctcaagtgagagc 357
QY      358  ggttcagagcagagctgagctgagctgagctgagctgagctgagctgagctgagctgagctgag 417
Db      358  ggttcagagcagagctgagctgagctgagctgagctgagctgagctgagctgagctgagctgag 417
QY      418  ctacttctgctgcttaccatctgacacacagcctccctctgcaagtaagtaagcagac 477
Db      418  ctacttctgctgcttaccatctgacacacagcctccctctgcaagtaagtaagcagac 477
QY      478  cctctgagatgagtgagaaagacatattgagtgagtgagtgagtgagtgagtgagtgagtgag 537
Db      478  cctctgagatgagtgagaaagacatattgagtgagtgagtgagtgagtgagtgagtgagtgag 537
QY      538  ccaagcgcctaatctatctgctgcttcaactgagctgagctgagctgagctgagctgagctgag 597
Db      538  ccaagcgcctaatctatctgctgcttcaactgagctgagctgagctgagctgagctgagctgag 597
QY      598  ggcagagtgatcagagcagagatctcaactgacacacacacacacacacacacacacacacacac 657
Db      598  ggcagagtgatcagagcagagatctcaactgacacacacacacacacacacacacacacacacac 657
QY      658  ggcagagtgatcagagcagagatctcaactgacacacacacacacacacacacacacacacacac 717
Db      658  ggcagagtgatcagagcagagatctcaactgacacacacacacacacacacacacacacacacac 717
QY      718  ctggaatacaaa 729
Db      703  ctggaatacaaa 714

RESULT 15
PCT-US00-19843-16
; Sequence 16, Application PC/TUS0019843
; GENERAL INFORMATION:
; APPLICANT: Herr, John C.
; APPLICANT: Norton, Elizabeth J.
; APPLICANT: Deikman, Alan B.
; TITLE OF INVENTION: Recombinant Antibody Directed Against Human Sperm
; FILE REFERENCE: 00415-02
; CURRENT APPLICATION NUMBER: PCT/US00/19843
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 60/145,512
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentlin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Mus musculus
PCT-US00-19843-16

```

```

Query Match      58.5%; Score 426.6; DB 1; Length 753;
Best Local Similarity 74.8%; Ptd. No. 8.3e-117;
Matches 550; Conservative 0; Mismatches 179; Indels 6; Gaps 1;

```

```

QY      1  caggtgacagctgacagcagcttgggagagctgtgtgaggtcaggggctcagtcaggtg 60
Db      7  caggtgacagctgacagcagcttgggagagctgtgtgaggtcaggggctcagtcaggtg 66
QY      61  tccctgacaaactctgcttcaacaatlaaagaacttctatatgacatggtgtaagcagaag 120
Db      67  tccctgacaaactctgcttcaacaatlaaagaacttctatatgacatggtgtaagcagaag 126
QY      121  cctgaacagagcctgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 180
Db      127  cctgaacagagcctgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 186
QY      181  gccccgaagttcagagcagaagcgaactatgactgacagacatctccctcaataagacctac 240
Db      187  gccccgaagttcagagcagaagcgaactatgactgacagacatctccctcaataagacctac 246
QY      241  ctgacagctcagcagcctgagatctgagagacacgctcccttattatgtaatttttaagg 300
Db      247  ctgacagctcagcagcctgagatctgagagacacgctcccttattatgtaatttttaagg 306
QY      295  taaggagatgcttggactattggagcagaagcagaagcagaagcagaagcagaagcagaagcaga 354
Db      307  taaggagatgcttggactattggagcagaagcagaagcagaagcagaagcagaagcagaagcaga 366
QY      355  ggcggttcagagcagagctgagctgagctgagctgagctgagctgagctgagctgagctgag 414
Db      367  ggcggttcagagcagagctgagctgagctgagctgagctgagctgagctgagctgagctgag 425
QY      415  ccaacttctgctgcttaccatctgacacacacagcctccctctgcaagtaagtaagcagac 474
Db      427  ccaacttctgctgcttaccatctgacacacacagcctccctctgcaagtaagtaagcagac 486
QY      475  agcctctgagatgagtgagaaagacatattgagatggtgttaccagagcagaagcaga 534
Db      487  agcctctgagatgagtgagaaagacatattgagatggtgttaccagagcagaagcaga 546
QY      535  tctccaaagcgcctaatctatctgctgcttcaactgagctgagctgagctgagctgagctgag 594
Db      547  tctccaaagcgcctaatctatctgctgcttcaactgagctgagctgagctgagctgagctgag 606
QY      595  actgagcagtgatcagagcagagatctcaactgacacacacacacacacacacacacacacacac 654
Db      607  actgagcagtgatcagagcagagatctcaactgacacacacacacacacacacacacacacacac 666
QY      655  ttggagatttatctgctgagcagaagttacacatctcccgctcaagctgagctgagcagc 714
Db      667  ttggagatttatctgctgagcagaagttacacatctcccgctcaagctgagctgagcagc 726
QY      715  aagctggaatacaaa 729
Db      727  aagctggaatacaaa 741

```

Search completed: February 18, 2001, 01:29:16  
 Job time: 18114 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2001, 13:14:09 ; Search time 83.91 seconds  
(without alignments)  
1400.141 Million cell updates/sec

Title: US-09-297-181-1

Perfect score: 729  
Sequence: 1 caggtcagctgcagctgcagctc.....gcaccagctcgaatcaaa 729

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/PCRTS.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/Dackfilest1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	435	59.7	907	3	US-09-184-658-9
2	432.2	59.3	810	2	US-08-652-507-1
3	425.2	58.3	1679	2	US-08-661-052-15
4	407.4	55.9	1095	3	US-08-875-811-52
5	407.4	55.9	1098	3	US-08-875-811-54
6	361.8	49.6	772	1	US-08-331-398A-33
7	361.8	49.6	772	2	US-08-331-397B-33
8	361.8	49.6	772	2	US-08-331-397B-33
9	352.4	48.3	720	2	US-08-800-198-7
10	352.4	48.3	720	3	US-09-296-595-7
11	349.2	47.9	1797	1	US-08-463-163-2
12	349	47.9	738	1	US-08-331-398A-31
13	349	47.9	738	2	US-08-331-397B-31
14	349	47.9	738	2	US-08-759-804A-31
15	347.6	47.7	719	3	US-08-279-772A-7
16	347.6	47.7	720	3	US-08-902-486-10
17	339.8	46.6	756	2	US-08-797-689-17
18	339.8	46.6	756	2	US-08-752-844-65
19	332	44.2	726	2	US-08-553-497A-25
20	318.2	43.6	2012	1	US-08-235-838-15
21	318.2	43.6	2012	2	US-08-465-473B-15
22	315.6	43.3	748	1	US-08-235-838-10
23	315.6	43.3	748	2	US-08-465-473B-10
24	312.2	42.8	831	2	US-08-403-853-17
25	308.2	42.3	732	2	US-08-553-497A-19
26	306.6	42.1	1065	3	US-08-875-811-56
27	305.6	41.9	336	2	US-08-678-194-5
28	305.4	41.9	354	3	US-08-767-128-21

29	305.2	41.9	924	2	US-08-860-174A-9	Sequence 9, Appl
30	305	41.8	726	2	US-08-553-497A-27	Sequence 27, Appl
31	302.4	41.5	336	3	US-09-184-658-11	Sequence 11, Appl
32	300.2	41.2	732	2	US-08-553-497A-21	Sequence 21, Appl
33	299.4	41.1	780	2	US-08-447-402-6	Sequence 6, Appl
34	298.8	41.0	797	2	US-08-894-922A-13	Sequence 13, Appl
35	297.6	40.8	2165	2	US-08-263-911-6	Sequence 6, Appl
36	297.6	40.8	2165	2	US-08-263-911-6	Sequence 8, Appl
37	297.2	40.8	891	2	US-08-894-922A-9	Sequence 9, Appl
38	290.6	39.9	738	2	US-08-553-497A-23	Sequence 23, Appl
39	288	39.5	1460	2	US-08-352-338A-18	Sequence 18, Appl
40	288	39.5	1460	3	US-09-166-750-18	Sequence 18, Appl
41	288	39.5	1460	3	US-09-166-093-18	Sequence 18, Appl
42	288	39.5	1460	3	US-09-172-019-18	Sequence 18, Appl
43	288	39.5	1460	3	US-09-166-094-18	Sequence 18, Appl
44	285	39.1	712	4	PCT-US92-08257-8	Sequence 8, Appl
45	284	39.0	858	2	US-08-428-257A-71	Sequence 71, Appl

## ALIGNMENTS

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RESULT 1
US-09-184-658-9
Sequence 9, Application US/09184658
Patent No. 6030792
GENERAL INFORMATION:
APPLICANT: Otterness, Ivan G.
APPLICANT: Mezes, Peter S.
APPLICANT: Downs, James T.
APPLICANT: Johnson, Kimberly S.
TITLE OF INVENTION: Assays for Measurement of Protein Fragments in
FILE OF INVENTION: Biological Media
CURRENT APPLICATION NUMBER: US/09/184,658
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/065,423
EARLIER FILING DATE: 1997-11-13
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentia Ver. 2.0
SEQ ID NO 9
LENGTH: 907
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 5109 VH - VL
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (29)-(94)
OTHER INFORMATION: Engineered signal peptide in pCANTAB6; initiator
OTHER INFORMATION: methionine is coded for most likely by gtc codon.
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (95)-(895)
OTHER INFORMATION: Coding sequence for genetically engineered single
OTHER INFORMATION: chain antibody - 5109 VH - VL.
US-09-184-658-9
Query Match
Best Local Similarity 59.7%; Score 435; DB 3; Length 907;
Matches 553; Conservative 0; Mismatches 175; Indels 3; Gaps 1;
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Db 216 cagacaaagagctggaagtgagtcgcaaccatattagtaagtggtctaccattatg 275
Qy 182 ccccgaaagtcacagcaagcaccatagctgacagacacatccccaacagcctacc 241
Db 276 cagacagtgtagaagggccgattacacattccagagaacaaatgcacaaacccctatc 335
Qy 242 tgcagctcagcagcctgacatctgagagacatgcgctattatattgtaattttacgggg 301
Db 336 tgcgaatgacagcagcgaagctcgtggagcaccagcagcatgtattactgtgaagaagata 395
Qy 302 atgcttgactatttgaggcgaagggcaccagctacacgctctctcagtgaggggcggtt 361
Db 396 gtaattacgcctgcgtgaggcgaagggcgctgctcactgctcagtgaggaggcggtt 455
Qy 362 caggcgagtgagctctgagcggtgagcgatcg---gatgtttgtagaccacacccac 418
Db 456 caggcgagtgagcagcgagcggtgagcgatcgctctatgttgtagagaccacacccac 515
Qy 419 tcaattgtcgtgttacatgagcaacacagcctcactctctgcaagtcgaagtcagagcc 478
Db 516 tcaattgtcgtgttacatgagcaacacagcctcactctctgcaagtcgaagtcagagcc 575
Qy 479 tcttgatagtgtagtgaagacatatttgaattggtgttacagagggccaagcagcttc 538
Db 576 tcttgatagtgtagtgaagacatatttgaattggtgtgttcagagggccaagcagcttc 635
Qy 539 caaagcgctaatctatctggtgtctcaactgagcctgagagcctctgcaagtcagcttc 598
Db 636 caaagcgctaatctctctggtgtctcaactgagcctgagagcctctgcaagtcagcttc 695
Qy 599 gcaatgagtcagaggaacatttcacacatgaacaaacagagtgagggcctgaggaattgg 658
Db 696 gcaatgagtcagaggaacatttcacacatgaacaaacagagtgagggcctgaggaattgg 755
Qy 659 gggattattatgtgtgcaaggaacacattctcgcctacagttcgtgtgtgagccaagc 718
Db 756 gggattattatgtgtgcaaggaacacattctcgcctacagttcgtgtgtgagccaagc 815
Qy 719 tgaagaatcaaa 729
Db 816 tggagctgaaa 826

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RESULT 2  
 US-08-652-507-1  
 ; Sequence 1, Application US/08652507  
 ; Patent No. 5876691  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN  
 ; TITLE OF INVENTION:  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Nixon & Vanderhye, P.C.  
 ; STREET: 1100 No. 5876691th Glebe Road, 8th Floor  
 ; CITY: Arlington  
 ; STATE: Virginia  
 ; COUNTRY: USA  
 ; ZIP: 22201-4714  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/652,507  
 ; FILING DATE: 02-Jul-1996  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Arthur R. Crawford  
 ; REGISTRATION NUMBER: 25,327  
 ; REFERENCE/DOCKET NUMBER: 117-211

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 810 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-652-507-1

Query Match 59.3%; Score 432.2; DB 2; Length 810;
Best Local Similarity 76.7%; Pred. No. 3.2e-118;
Matches 568; Conservative 0; Mismatches 143; Indels 30; Gaps 2;

Qy 1 cagggtgacgtcagcagcgtctggtgcaagagctgtgaggtcaggggcccacagtcagttg 60
Db 79 CAGGTGAACCTCCACAGCTGGGCGAGAACTGTGAGTCAAGGACCTCACTCAAGTTG 138
Qy 61 tcttcacagctctggtctcaacattaaagactaatatgacatgagtgagtcagagag 120
Db 139 TCTTCACAGCTTCTTGCTTCAACATTAAAGCTCTTATATCAGTGTGAGCGAGGG 198
Qy 121 cctgaaacagggcctgagtgatgtgattgattgatacctgaaatgagtcagatat 180
Db 199 CCTGAACAGGGCTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 258
Qy 181 gcccgaagttccaaagggcagcagcactatgactgagagacactcctccaatcagctac 240
Db 259 GCCCGGAATTCAGAGGGCAGGCACTTTACTACAGACACTCTCCAAACACACCTTAC 318
Qy 241 cgcagcctcagagcctgagcctgagcagcagcagcagcagcagcagcagcagcagcagc 291
Db 319 CTGCACTCAGCAGCTTGTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 378
Qy 292 ----tttcagggatgcttggactattggggccaagggcagcagcagcagcagcagcagc 348
Db 379 CCGACTGGGCGCTACTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 438
Qy 349 ggtgagagcgttcagagggaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 408
Db 439 GGTGAGAGCGGTTCAAGCGGAGGTGCTGTGGGTGGCGGATCGAATAATGTGCTCAC 498
Qy 409 caaatccacactcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 468
Db 499 CAGTCTCCAGCATATATGTCTCATCTCCAGGGAGAGAGTACCATTAACCTGAGTGGC 558
Qy 469 agtcagagcctctgtagatgtgtagaagacatatgtgaattgtgtgttcaagagccaa 528
Db 559 AGCTCAAGTGA-----AGTTACATGACATGCTGCTCAGCAGAACCA 600
Qy 529 ggcacgtctcacaagcgctaatctatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 588
Db 601 GGCACGTTCTCCCAAACTGTGATTTATGACACATCAACCTGGCTTTCGAGATCCCTCT 660
Qy 589 agttcactgagcagtgagtcagagcagagatttcacacagcgaatacaagaagtgaggct 648
Db 661 CGCTTCAGTGCAGTGTGATCTGAGACCTTACTCTTCTCAGCATATAGCCGAAATGAGGCT 720
Qy 649 gaggatttggagattatattgtgtgcaaggtacacattctcgcctcagcttgcgtgtgt 708
Db 721 GAAGATGTGCGCATTATTATAGCCAGAGAGAGTATGATACCCACTACGTTGGTGTCT 780
Qy 709 ggcaccaagctggaatacaaa 729
Db 781 GGCACCAAGCTGAGCTGAAA 801

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RESULT 3  
 US-08-661-052-15  
 ; Sequence 15, Application US/08661052

Patent No. 5837243  
GENERAL INFORMATION:  
APPLICANT: Yashwant M. Deo  
APPLICANT: Joel Goldstein  
APPLICANT: Robert Graziano  
APPLICANT: Ch�lian Somasundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/661,052  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/484,172  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1679 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 11..1667  
US-08-661-052-15

Query Match 58.3%; Score 425.2; DB 2; Length 1679;  
Best Local Similarity 76.4%; Pred. No. 5e-116;  
Matches 561; Conservative 0; Mismatches 143; Indels 30; Gaps 2;

QY 8 agctgcagcagcttggtggcagagcttctgagctcagggcctcagtaattgtctgca 67  
DB 846 AACTGCGAGCGAGTGTGGGCGAGAACTTGTGAGGTGAGGAGCTTCAAGTTGCTGCA 905  
QY 68 cagcttcgtgcttcaataaataaactactatatactgacgtgtgaagcagagccctgaac 127  
DB 906 CAGCTTGTGCTTCAACATTAAGACTCCATATGCACTGTGAGGCAAGGCGCTGAAC 965  
QY 128 agggcctgagtgatgagctgagctgagctgagaaatgggtgatactgaatgccccga 187  
DB 966 AGGGCCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1025  
QY 188 agttcagggcagagcactatgactcagacacacatctccatacagcttaccctgagc 247  
DB 1026 AGTTCCAGGGCAGGCGCACTTTTACTACAGACACATCCTCAACACAGCCTACTGAGC 1085  
QY 248 tcagcagccctgagcactgagagacactgcgtctatattgttaat-----ttt 295  
DB 1086 TGAGCAGCCTGACATCTGAGGACACTGCCGTCTATTATTGTAATGAGGAGACGCCACTG 1145  
QY 296 acgggagatgcttgagctatttggtggcagagacacagctcacgctctcctcagtgag 355

DB 1146 GGCCGACTACTTTGACTACTGAGGCGCAAGGACCAAGGCTACCGCTCTCCAGGTGAG 1205  
QY 356 gcggttcagggaggtggtctgscggtgsggagtcggatgtttgatacccaacac 415  
DB 1206 GCGGTTCAGGCGAGGTGCTGTGGGGGTGCGGATCAGAAATGCTCACCAGTCTC 1265  
QY 416 cactcattgctcggttacattgagcaaacagccctcactccttcctgcaatgacaga 475  
DB 1266 CAGCATCATGCTGTGATCTCCAGGAGAGAGTCAACCAATACCTGCACTGCACTCA 1325  
QY 476 gctccttgatagtgatgagaaacatattgaattggtgttcaagagccagccagt 535  
DB 1326 GTGTA-----AGTTACATGCACTGTGTCAGAGCAAGCCAGGCACACTT 1367  
QY 536 ctccaaagccctaatctatctcgtgtgtcctaactgacctgagtcctcagcaagttca 595  
DB 1368 CTCGCCAACTGTGATTATTAACACATCCAACTGAGCTTGTGAGTCCCTGCTCGCTTA 1427  
QY 596 ctggcagtgatcagaggaatttcacacitgaataacacagagtgaagctgagalt 555  
DB 1428 GTGGCAGTGTGATCTGGGAGCTCTTACTCTCTCAATACGCGGAGTGAAGATG 1487  
QY 656 tgggagttatattgctggaaggtacacattctccgtcagcttggtgctgcaccca 715  
DB 1488 CTGCCACTTATTACTGCCAGCAAGGAGTAGTTACCCACTCAGTTCGCTGCTGCACCA 1547  
QY 716 agctggaatacaaa 729  
DB 1548 AGCTGGAGCTGAAA 1561

RESULT 4  
US-08-875-811-52  
Sequence 52, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Bogue, Lluís  
APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Fairis, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:

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; LENGTH: 1095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1095
; OTHER INFORMATION: /note="Metseronc87FBMC31"
US-08-875-811-52

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Query Match      55.9%; Score 407.4; DB 3; Length 1095;
Best Local Similarity 72.4%; Pred. No. 7.3e-111;
Matches 528; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

QY 1 caggtgacgttcagcagcgtctggcgagcctgtgtgagtcagggcctgaatcttg 60
DB 355 CAGGTGAAGCTGCGAGCGGTGAGGAGCTGAGAGAGGCTGAGAGAGAGAGAGAGATC 414
QY 61 tccctgcacagcttcgtgctcaacatlaagactactatctgactgtgtgaagcagag 120
DB 415 TCCTGCAAGGCTTCTGGGTACACCTTCAAACTAGATGAATGAAGTGGTGAAGCAGCT 474
QY 121 cctgaacagggcctgagtgatgtgagtgatgtgactcctgaagatgtgataat 180
DB 475 CCAGGAAGGCTTAAAGTGGATGGGCTGATTAACCTCACTGAGAGTCAACATAT 534
QY 181 gccccgaagttccagggcagggccactatgacagcagacacatccctcaataagcctac 240
DB 535 GCTGATGACTTCAAGGAGCGGTTTGCCTTTCTTCTAGAAAACCTGCGAGCGTCCCTAT 594
QY 241 ctgcagctcagcagcagctgcacatctgaagacactgcgctcatatattgttaatttca 300
DB 595 TTGCAATCAACAACCTCAAAAATGAGAGACAGCGGTACATATTTCTGTGAAGATTGCT 654
QY 301 gatgcttgactatctggggcagggcagggcagggcagggcagggcagggcagggc 360
DB 655 ATTAAGGGGACTACTGGGGCCAGAGGACACGCTACCTCTCTCAGGTGAGGGGCT 714
QY 361 tccagggcagggcagggcagggcagggcagggcagggcagggcagggcagggcagggc 420
DB 715 TCGAGCGGAGGCTGCTTGGCGGTGGCGGATCGGACATTTGCTTACCCAGCTCCATTC 774
QY 421 acttctgcttaccatctgacacacacacacacacacacacacacacacacacacac 480
DB 775 TCCATTCAGTCACTCTTGGAATCATGCTTCATCTCTGCAAGGCTCAAGAGCTC 834
QY 481 ttgataagtgatgaagaacataatttgatgtgtttaaagggcagggcagggcagggc 540
DB 835 CTACATAGTATGACATCACTTATTTGTATGATCTGCAAGAGCCAGCCAGTCTCCT 894
QY 541 aagcgcctaatctatctggtgtcctaaactgactgagtcctcctcagggcagggcagggc 600
DB 895 CACCTCTCTGATTTATCAGATGCTCAACCTTGCTCAGAGATCCCAAGACAGTTCAGAGC 954
QY 601 agtgcagcagggcagggcagggcagggcagggcagggcagggcagggcagggcagggc 660
DB 955 AGTGGGTCAAGAGACTGATTTCAACTGAGATCAGAGTGAAGGAGGCTGAGATGGGGT 1014
QY 661 gttattatctgctggcagggcagggcagggcagggcagggcagggcagggcagggc 720
DB 1015 GTTATTACTGCTCTCAAAATCTAGAAATTCCTGCGACGCTTGGTGAAGCCACCAAGCTG 1074
QY 721 gaaatcaaa 729
DB 1075 GAAATCAAA 1083

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RESULT 5
US-08-875-811-54
; Sequence 54, Application US/08875811
; Patent, No. 6045793

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```

; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Diane L.
; APPLICANT: Bogue, Luis
; APPLICANT: Miodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1098 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1098
; OTHER INFORMATION: /note="MOC31FBmetseronc"
US-08-875-811-54

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Query Match      55.9%; Score 407.4; DB 3; Length 1098;
Best Local Similarity 72.4%; Pred. No. 7.3e-111;
Matches 528; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

QY 1 caggtgacgttcagcagcgtctggcgagcctgtgtgagtcagggcctgaatcttg 60
DB 4 CAGGTGAAGCTGCGAGCGGTGAGGAGCTGAGAGAGGCTGAGAGAGAGAGAGATC 63
QY 61 tccctgcacagcttcgtgctcaacatlaagactactatctgactgtgtgaagcagag 120
DB 64 TCCTGCAAGGCTTCTGGGTACACCTTCAAACTAGATGAATGAAGTGGTGAAGCAGCT 123
QY 121 cctgaacagggcctgagtgatgtgagtgatgtgactcctgaagatgtgataat 180
DB 124 CCAGGAAGGCTTAAAGTGGATGGGCTGATTAACACTTACACTGAGAGATCAACATAT 183
QY 181 gccccgaagttccagggcagggccactatgactgacagacacatccctcaataagcctac 240
DB 184 GCTGATGACTTCAAGGAGCGGTTTGCCTTTCTTCTAGAAAACCTGCGCGCTGCTAT 243
QY 241 ctgcagctcagcagcagctgcacatctgaagacactgcgctcatattgttaatttca 300
DB 244 TTGCAATCAACAACCTCAAAAATGAGAGAGCGGCTTACTATTTCTTGTGCAAGATTGCT 303

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OY	301	gatccttggagcattttggccaagaggaaccaaggttaacacgtccctcaagttgagagcgt	360
Db	304	ATTAAAGGGGGACTACTGGGGCCAAAGGACACAGGTCAACGCTCTCTTCAAGTGGAGCGGT	363
OY	361	tcaagcggagatgtagctctgcgcgtgtgcgatalcggatgltttgatgaccacaactcacctc	420
Db	364	TCAGCGGAGAGGTGGCTCTGCGGGTGCGGAGATCGGAGATTTGGTAAACCCAGTCTTCATTC	423
OY	421	actttgtcgtgttacattgggaacacagccctccctctcttcgaaatgaatgcagagctc	480
Db	424	TCCAAATCCAGTCACCTCTTGGAACTACAGCTCTCACTCTCTGACAGGTCTACTAAAGTCTC	483
OY	481	ttggatagtgatggaaaagacaatttggatttgttgcataagagagcgcaagccagctccca	540
Db	484	CTACATACTAATGGCATCATTATTGTGATGTGATGTGCGAAGGCCAGGCACTCTCCT	543
OY	541	aagcgccatactatctcgtgtgtctaactgtaacctctggagctccctgacaggttaactcgtc	600
Db	544	CAGCTCCGATTATTTCACATGTCTCAACCTTCCCTCCAGAGGCCAGACAGGTTCTAGTAGC	603
OY	601	agttgatacaggagaacgattccacactgaaatacaacagagatggagagtgtsagatttggga	660
Db	604	AGTGGGTACGAACTGATTTCACACTGGAATTCAGCAAGTGGAGGCTTGAGAGATGTGGGT	663
OY	661	gttatttatgtcgtgcaaggtacacatctccgcctcaagtcggtcgtgtgtcgtggacccaagctg	720
Db	664	GTTTATTACTGTGCAAAATCTTGAAATTTCTCTGGAGCTTGGGTGGAGGCGACCAACACTG	723
OY	721	gaaatcaaa 729	
Db	724	GAAATCAAA 732	

RESULT 6  
 US-08-331-398A-33  
 Sequence 33, Application US/08331398A  
 Patent No. 5608039  
 GENERAL INFORMATION:  
 APPLICANT: Pastan, Ira  
 APPLICANT: Willingham, Mark  
 APPLICANT: Fitzgerald, David  
 APPLICANT: Brinkmann, Ulrich  
 APPLICANT: Pal, Lee  
 TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins  
 TITLE OF INVENTION: and Their Uses (as amended)  
 NUMBER OF SEQUENCES: 68  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew  
 STREET: One Market Plaza, Stewart Street Plaza  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94105-1492  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/331,398A  
 FILING DATE: 28-OCT-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/767,331  
 FILING DATE: 30-SEP-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/596,289  
 FILING DATE: 12-OCT-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hunter, Tom  
 REGISTRATION NUMBER: 38,498  
 REFERENCE/DOCKET NUMBER: 015280-12611005

```

1 TELECOMMUNICATION INFORMATION:
2 TELEPHONE: (415) 543-9600
3 TELEFAX: (415) 543-5043
4 INFORMATION FOR SEQ ID NO: 33:
5 SEQUENCE CHARACTERISTICS:
6 LENGTH: 772 base pairs
7 type: nucleic acid
8 STRANDEDNESS: single
9 TOPOLOGY: linear
10 MOLECULE TYPE: DNA
11 FEATURE:
12 NAME/KEY:
13 LOCATION: 1..772
14 OTHER INFORMATION:
15 OTHER INFORMATION:
16 OTHER INFORMATION:
17 OTHER INFORMATION:
18 OTHER INFORMATION:
19 FEATURE:
20 NAME/KEY: CDS
21 LOCATION: 27..770
22 US-08-331-398A-33

```

Query Match	49.6%	Score 361.8	DB 1	Length 772
Best Local Similarity	69.3%	Pred. No. 1.7e-97		
Matches 511	Conservative 0	Mismatches 217	Indels 9	Gaps 1
Qy	2	aggctgacgctcgcagcagctctgggcagagactgtgtgagtcagagggccctcagtcaggttgt	61	
Db	31	ATGTAACTGTGTGGAGTCTGGGGGAGGGCTTAGTGCACGCTGGAGGGTCCCGAAACTCT	90	
Oy	62	cctgcacagctctctggtcttcaacatlaaagactactatatgcactgggtgaagcagagc	121	
Db	91	CCTGTGCACACTCTGTGATTCACTTTCACGTGACTATTATCATGTATGTGGGTTCGCCAGACTC	150	
Oy	122	ctgaacagagccttgagatgagatttgatgatgatcccggaatgtgatgactgatatgt	181	
Db	151	CAGAGAAAGGCTGTGAGTGGTGCCGATCATTTAGTATGATGATGATGTCGCCGCTTATT	210	
Oy	182	ccccgaagcttcagagggcagagccactatgactctgacacacatccctacatacagctacc	241	
Db	211	CAGACACGTAAAGGCGGGTTACACATCTCCAGACAAATGCCAGGAACACCCCTTAC	270	
Oy	242	tgcagctcagagagccctggcatctgagagcaactgcccgtctatattgt-----aalt	292	
Db	271	TGCAATAGGCGGTGTGAAGTCTGAGACACAGCCATATATCTGTGCAAGAGGACTGG	330	
Oy	293	tttaaggagatgctttgactatttggggccaaagggacacaggtaccgctctcctaagt	352	
Db	331	CCTGGGGAGCCGTGTCTTCTTACTGTGGGGCAAGGGACCTGGTCACTGTCTTCAGGCG	390	
Oy	353	gagagggatcagggaggtgtgctgtgcggttgaggatcgagattttgattgaccacaa	412	
Db	391	GAGCGGATCCGGTGTGTGGGATTTGGAGTGGCGGAAGCGATGTGCTGATGACCCAGT	450	
Oy	413	ctccactaccttgcgttaccattcattgacacacaccgctccatcccttgcgaatgaatc	472	
Db	451	CTCCATTGAGTTTACCTGTCACTGATCTTGGAGATCAAGCCCTCATCTCTTGAGATCTAGC	510	
Oy	473	agagccctcttgatagtgtatggaagacatatattgaaattgtgtttacagagggccagcc	532	
Db	511	AGATATTGTACATGTATGATAAGAAACACCTATTATTGAAATGTATCTTGAGAAACAGGCC	570	
Oy	533	agtcaccaagcgccctaactatctatctgctgtctaaactgagactcttgagctccctgacagt	592	
Db	571	AGTCTCCAAAGCTCTGTGATCTACAAAGTTTCCAAACCGATTTTCTTGGGGTCCAGACAGCT	630	
Oy	593	tcaactggcagtgatcagagacagattccacactgaaataatcaacagagttgaggtctgag	652	
Db	631	TCAGTGGCAGTGGATCAGGAGACAGATTTCACACTCAAGATCAGCAGAGTGGAGGCTGAGG	690	
Oy	653	attgggagttatatattgtctggcagagtlacacatctccgctcagttcggttgctgca	712	



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1      COMPUTER READABLE FORM:
2      MEDIUM TYPE: Floppy disk
3      COMPUTER: IBM PC compatible
4      OPERATING SYSTEM: PC-DOS/MS-DOS
5      SOFTWARE: Patent In Release #1.0, Version #1.30
6
7      CURRENT APPLICATION DATA:
8      APPLICATION NUMBER: US/08/759,804A
9      FILING DATE: 03-DEC-1996
10     CLASSIFICATION: 536
11
12     PRIOR APPLICATION DATA:
13     APPLICATION NUMBER: US 08/331,358
14     FILING DATE: 28-OCT-1994
15
16     PRIOR APPLICATION DATA:
17     APPLICATION NUMBER: US 07/767,331
18     FILING DATE: 30-SEP-1991
19
20     PRIOR APPLICATION DATA:
21     APPLICATION NUMBER: US 07/596,289
22     FILING DATE: 12-OCT-1990
23
24     ATTORNEY/AGENT INFORMATION:
25     NAME: Weber, Ellen L.
26     REGISTRATION NUMBER: 32,762
27     REFERENCE/DOCKET NUMBER: 015280-126140US
28     TELECOMMUNICATION INFORMATION:
29     TELEPHONE: (415) 576-0200
30     TELEFAX: (415) 576-0300
31
32     INFORMATION FOR SEQ. ID NO. 33:
33     SEQUENCE CHARACTERISTICS:
34     LENGTH: 772 base pairs
35     TYPE: nucleic acid
36     STRANDEDNESS: single
37     TOPOLOGY: linear
38     MOLECULE TYPE: DNA
39
40     FEATURE:
41     NAME/KEY: -
42     LOCATION: 1..772
43
44     OTHER INFORMATION:
45     OTHER INFORMATION: protein of B3 monoclonal antibody
46     OTHER INFORMATION: Variable Heavy chain (V-H) and Variable
47     OTHER INFORMATION: Light chain (V-L) Fv region joined by a
48     OTHER INFORMATION: (gly-4ser)-3 peptide linker".
49
50     NAME/KEY: CDS
51     LOCATION: 27..770
52
53     LOCATION: 27..770
54     US-08-759-804A-33

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US-08-759-804A-33

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Query Match 511: 49.6%; Score 361.8; DB 2; Length 772;
Best Local Similarity 69.3%; Pred No. 1.7e-97;
Matches 511; Conservative 0; Mismatches 217; Indels 9; Gaps 1

QY 2 aggtcagctgcaagcagctctgggccaagactgtgtgagtcgaagggccctcagtcgaattgt 61
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 31 ATGTGAAGCTGTGTGAGTGTGGGGGAGCCTTATGTGACAGCTGGAGGGTCCCTGAACCT 90
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 62 cctgcacagctctctggtcttcaacaatlaaagactatataatgcactgctggtgtgaagcaagc 121
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 91 CCTGTGCACACCTCTGGATTCACTTTCAGTGACATTACATGTGTTGGGTCCGCAACACT 150
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 122 ctgaacagggccttgtagtgatgtgtgtatgtatctctgaagatggtgatacgaatay 181
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 151 CAGAGAAAGAGGCTGTGGATGTGGTGGCTACATTATGATATGATATGTTCCGCGCTATT 210
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 182 ccccgcaagttccacaggccaagggccactatgacatgcagacacatctccatatacagcttacc 241
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 211 CAGACACTGTAAAGGCGGTTCCACCATTCACAGACACATGCAAGAACACCCCTCTACC 270
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 242 tgcagctcagcagcctgagcatctagagacactgcegtctattatgtt-----aatt 292
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 271 TGCAAATGAGCCGCTGTGAAGTCTGAGAGACACACCCTAATATTCCTGTGCAAAGAGACTGG 330
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 293 tttaagggatctcttgagactatttgggccaaggggccaagggccacggtcctctctgagtg 352
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 331 CCTGGGGAACCTCGTGTCTTACTGTGGGGCCAAAGGAGCTGTGGTCACTGTCTCTCAAGGC 390
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OY      353   gagcgagtcaggagggagtggtgcttgcggcgtgacggatcgtattgttaaccacaa 417
          |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      351   GAGCGGATCCGGTGTGTGGCGCATCTGGAGGTGGCGAAGCAGATTGTCTATTAACCAAGT 450
          |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY      413   ctccactactttgtcggttaccaatlggaacaacagacctcatctcttgagaatcaagt 472
          |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      451   CTCATTAGTTTACGTGCAGTGCTTGGAGATCAAGCCTCCATCTCTTCAGATCTTAGTC 510
          |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY      473   agagcctcttgatagtatgatgaaagacatatltgaaatttgttgtttaagaagcccagcc 532
          |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      511   AGATCATGTGTCAATAGTAATGGAACAACACTATTTAGATGTGTACCTGCACAAACCAGGCC 570
          |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY      533   agctccaagcgcgcatactatctggctgtctaactaacctgagactctgagctccctgacagt 592
          |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      571   AGTCTCCAACACTCTCTGATCTACAAAGTTTCCAACCCATTTTCTGGGGTCCACAGACAGT 630
          |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY      593   tcaactgagcagtgatlcagagacagatttccactgtaaatacaacagatlgagagctgag 652
          |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      631   TCAGTGGCAGTGAATACAGGACAGATTTCAOACTCAAGATCAGACAGAGTGAGAGCTGAGG 690
          |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY      653   attggagagtttatattgtctgccaagytacaaatctccgtcacgttctgtgtctggca 712
          |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      691   ATCTGGGGATTATTACTGCTTTCAAGGTTCAATGTTCATTCATTCACGTTGGCTCGGGGA 750
          |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY      713   ccaagctggaatcaaa 729
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      751   CAAAGCTGGAATTTAAA 767
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

RESULT      9
US-08-800-198-7
Sequence 7, Application US/08800198
Patent No. 5942602
GENERAL INFORMATION:
APPLICANT: WELS, WINFRIED S.
APPLICANT: SCHMIDT, MATTHIAS
APPLICANT: VAKALOPOULOU, EVANGELIA
APPLICANT: SCHNEIDER, DOUGLAS
TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: MILLEN, WHITE, ZEILANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentlin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,198
FILING DATE: 13-FEB-1997
CLASSIFICATION: 530
..ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: SCH 1576
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HIPOTHEICAL: NO
ANTI-SENSE: NO

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CLASSIFICATION: 536
Prior Application DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
Prior Application DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
Prior Application DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-126140US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..738
OTHER INFORMATION: /note="Humanized B3 single-chain Fv"
US-08-759-804A-31

Query Match: 47.9%, Score 349; DB 2; Length 738;
Best Local Similarity: 68.2%; Pred. No. 9.9e-94;
Matches 503; Conservative 0; Mismatches 225; Indels 9; Gaps 1

QY 2 aggtcagctgcagcagcgtctggtggcagagcctgtgtagtcgaagggcctgaagctgtg 61
DB 2 atgtgaacctggtggagctctggggagcgcgtgctcagcccgccgctccctgaaacctt 61
QY 62 cctgcagcgtctctgtctgcacatcaataagactatatactgcactggtgtgaagcaagc 121
DB 62 cctgtgcacacctctgattcacttcttcacagcattattacattgatttgggtcccgagccc 121
QY 122 ctgaacagggcctgtagtggatttgatggattgactgcctcgtagaatggtgatactgaatg 181
DB 122 cggcgcaaggcctgtagtggatttgatggattgactgcctcgtagaatgattgattccggcttatt 181
QY 182 ccccgaaattccagggcgaagggccactatgactgcagacacacatccccaatacaagcttacc 241
DB 182 cagacacgttaaaaggccgggttcacacatctctagaagacatatgaacaaagacacccctctacc 241
QY 242 tgcagctcagcagcgtctgcatctcgtggagacatgcgcgtctattatgtt-----aatt 292
DB 242 tgcgaattgaatcgtgttcgcgcgcgcgcgagacacacacccattattatttccttcgaagaagactgg 301
QY 293 tttaagggaatgcttttgactatttggggccaaaggagaccaggttcaacgctctcctcagtg 352
DB 302 cctggggagaccctggtttgcttactggggccaaaggagaccctggttcaacgctctcctcagtg 352
QY 353 gaggcggttcagggcggaagtgtgctctctgcgcgtgtggcggaatcgagatgttttgatgagcccaa 412
DB 353 gaggcggttcagggcggaagtgtgctctctgcgcgtgtggcggaatcgagatgttcgtagaccacaat 421
QY 413 ctccactcactcttgcggtttacactatgggcaacacacagccctccactctcttgaagcaagtc 472
DB 413 ctccactcactcttgcggtttacactatgggcaacacacagccctccactctcttgaagcaagtc 472
QY 422 ctccatttgaatttacctgtgcaccccgccggagagaccggcctccattcttccagatctttagtc 481
DB 422 ctccatttgaatttacctgtgcaccccgccggagagaccggcctccattcttccagatctttagtc 481
QY 473 agagcctcttgatagtgatggaaagacatatlttgatgtgtgttgcacagagccagcc 532
DB 473 agagcctcttgatagtgatggaaagacatatlttgatgtgtgttgcacagagccagcc 532
QY 482 agatcatgtgacatgtgatatggaaacacctatttttgaatggtacacgacagacacggcc 541
DB 482 agatcatgtgacatgtgatatggaaacacctatttttgaatggtacacgacagacacggcc 541
QY 533 agtctccaaaggcctaatctatctcgtgtgtcctaaacttgagccttgagtccttgaaagt 592
DB 533 agtctccaaaggcctaatctatctcgtgtgtcctaaacttgagccttgagtccttgaaagt 592

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Db 542 AGTCTCCACAGCTGCTGATCTACAAAGTTTCCAAACCGATTTTCGTGGGCTCCACAGACAGT 601  
 QY 593 tcaatgacagtgatcagagacagattccacactgaatacaagaagtgaagctgaag 652  
 Db 602 TCAGTGGCAGATGATTCAGGAGACAGATTTCACACTCAAGATCAGAGAGTGGAGCTGAG 661  
 QY 653 attggagattatattgtctggaaggtacacattccgctcaagctgagctgga 712  
 Db 662 AGCTCGAGATTATTACTGCTTCAAGGTTACATGTTTCATTCACGTTGCGCAGGGTA 721  
 QY 713 ccaagctggaatcaaa 729  
 Db 722 CCAAGGTGAATTAA 738

## RESULT 15

US-08-279-772A-7  
 Sequence 7, Application US/08279772A  
 Patent No. 6080560

## GENERAL INFORMATION:

APPLICANT: Russell, David R  
 APPLICANT: Fuller, James T  
 TITLE OF INVENTION: Method for Producing Antibodies in Plant  
 NUMBER OF INVENTION: 9  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Quarles and Brady  
 STREET: PO Box 2113  
 CITY: Madison  
 STATE: WI  
 COUNTRY: United States of America  
 ZIP: 53701-2113

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/279,772A  
 FILING DATE:

## CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Seay, Nicholas J.  
 REGISTRATION NUMBER: 27,386  
 REFERENCE/DOCKET NUMBER: 11-229-9097-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 608-251-5000  
 TELEFAX: 608-251-9166

## INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 719 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:

NAME/KEY: CDS  
 LOCATION: 1..719  
 US-08-279-772A-7

Query Match 47.7%; Score 347.6; DB 3; Length 719;  
 Best Local Similarity 68.8%; Prid. No. 2.5e-93;  
 Matches 501; Conservative 0; Mismatches 209; Indels 18; Gaps 1;

QY 1 caggctcagctcagcagctgagggcagagctgtgaggtcagggcctcaagctg 60  
 Db 7 CAGGTCCAGCTTCAGAGTCTGGGCTGAAGTGGCAAAACCTGGGGCTCAGTGAAGATG 66  
 QY 61 tcctgacagctctgctcctcaacattaaagactatagctagctgggtgaagcagag 120  
 Db 67 TCCTGCAAGGCTTCTGCTACACCTTTACTAGTACAGATGCACTGGGTAAACAGAGG 126

QY 121 cctgaacagggccttgagtgatgagtgatgagtgatgagtgatgagtgatgagtgat 180  
 Db 127 CTGGACAGGGCTCTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 186  
 QY 181 gccccgaagttcaggcaggcaggcaggcaggcaggcaggcaggcaggcaggcaggcagg 240  
 Db 187 AATCAGAAAGTTCAAGAGCAAGGACACATTCAGTGCAGAGCAAAATCTCCAGCAGCTAC 246  
 QY 241 ctgacgtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300  
 Db 247 ATCAACTGAGAGAGCTGAGATTTGAGAGACTGAGAGACTGAGAGACTGAGAGACTGAG 306  
 QY 301 gatgcttgagtgatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 360  
 Db 307 GGGGTCTTGACACTACTAGGGGCAAGGACCACTCAGTCTCTCTCGGAGGGGCTGGC 366  
 QY 361 tcagggagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 420  
 Db 367 TCGGGGGGTGGCGCTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGG 426  
 QY 421 acttgctggtacattgagac 480  
 Db 427 ATCATGCTGATCTCCAGGGAGAGGTCCACATACCTGAGTCCAGCTCAAGTATA 486  
 QY 481 ttgagatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 540  
 Db 487 -----AGTTACATGACACTGCTCCAGCAGAGAGGACGACTTCTCC 528  
 QY 541 aagcgtacatcatctgtgttcaactgagctgagtgagtgagtgagtgagtgagtgag 600  
 Db 529 AAACCTGGATTATACACATCAACCTGGCTTGGAGTCCCTGCTGCTTCACTGAG 588  
 QY 601 agtgaatcagtgacagattcagacacgaaatcaacagagtgagtgagtgagtgagtg 660  
 Db 589 AGTGAATCTGGAGCTTACTTCTCAGATGAGGCAATGAGGCTGAGTGTGCC 648  
 QY 661 gttattatgtctgcaaggtacacattccgctcagctgagtgagtgagtgagtgagtg 720  
 Db 649 ACTTATTACGCGCATCAAGAGAGTACTTACCCACTCAGCTCGTTCGTTCTGGACCAAGCTG 708  
 QY 721 gaatacaa 728  
 Db 709 GAGGTCAA 716

Search completed: February 17, 2001, 22:59:21  
 Job time: 35112 sec

A;Reference number: JC5322; MUID:97168950

A:Accession: J03322  
 A:Molecule type: mRNA  
 A:Residues: 1-233 <TAN>  
 A:Experimental source: hybridoma cell  
 C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 64.6%; Score 832.5; DB 2; Length 233;  
 Best Local Similarity 68.9%; Pred. No. 1.5e-52;  
 Matches 164; Conservative 25; Mismatches 44; Indels 5; Gaps 3;

QY 5 QQSAAELVRSASVYKLSCTASGFNINQDYMHVYKORPEQGLEWIGMDPENGEYAPKF 64  
 DB 1 QESAAELVRSASVYKLSCTASGFNINQDYMHVYKORPEQGLEWIGMDPENGEYAPKF 60  
 QY 65 QGKATMTADTSSNTAVYLOLSLASEDTAVYCYCNFYGDALDVGOGTYVTVSSGGSGGG 124  
 DB 61 GVKATMTADTSSNTAVYLOLSLASEDTAVYCYCNFYGDALDVGOGTYVTVSSGGSGGG 117  
 QY 125 GSGGGSDVLTOTPLTSLVITIGOPASISCKSSQSLSDSGKTYLNLQRPQSPKRLI 184  
 DB 118 ASGGGSDIELTQSPASISCKSSQSLSDSGKTYLNLQRPQSPKRLI 176  
 QY 185 YLVSKLSDGVPRDTGSGSDFTLTKINRYEADLVGYVYCMOGTHSPLEAGTKLEI 242  
 DB 177 YLVNLSGVPARFSGSGSDFTLTKINRYEADLVGYVYCMOGTHSPLEAGTKLEI 233

## RESULT 3

A56446  
 Ig heavy chain V region (3H-3H scfv) - mouse (strain BALB/C)

C:Species: Mus musculus (house mouse)  
 C:Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996  
 C:Accession: A56446  
 R:Lang: P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.  
 J. Biol. Chem. 270, 7829-7835, 1995  
 A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical  
 A:Reference number: A56446; M01D:95229583  
 A:Accession: A56446  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-268 <TAN>  
 A:Cross-references: GB:U20617  
 C:Keywords: heterotrimer; immunoglobulin

Query Match 63.2%; Score 815; DB 2; Length 268;  
 Best Local Similarity 64.5%; Pred. No. 3.2e-51;  
 Matches 158; Conservative 30; Mismatches 49; Indels 8; Gaps 3;

QY 1 QVQLQSGAEIVRSASVYKLSCTASGFNINQDYMHVYKORPEQGLEWIGMDPENGEYAPKF 60  
 DB 3 QVQLQSGAEIVRSASVYKLSCTASGFNINQDYMHVYKORPEQGLEWIGMDPENGEYAPKF 62  
 QY 61 APRFQGAATMTADTSSNTAVYLOLSLASEDTAVYCYCNFYGDALDVGOGTYVTVSSGG 118  
 DB 63 DPRFQGAATMTADTSSNTAVYLOLSLASEDTAVYCYCNFYGDALDVGOGTYVTVSSGG 122  
 QY 119 GSGGGSDVLTOTPLTSLVITIGOPASISCKSSQSLSDSGKTYLNLQRPQSPKRLI 178  
 DB 123 GSGGGSDVLTOTPLTSLVITIGOPASISCKSSQSLSDSGKTYLNLQRPQSPKRLI 176  
 QY 179 SPRLIYLVSKLSDGVPRDTGSGSDFTLTKINRYEADLVGYVYCMOGTHSPLEAGTKLEI 238  
 DB 177 SPRLIYLVSKLSDGVPRDTGSGSDFTLTKINRYEADLVGYVYCMOGTHSPLEAGTKLEI 236  
 QY 239 KLEIK 243  
 DB 237 KLEIK 241

RESULT 4  
 C32513

Ig kappa chain precursor V region (BXMI4) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jan-2000  
 C:Accession: C32513  
 R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.  
 J. Clin. Invest. 82, 852-860, 1988  
 A:Title: Immunoglobulin kappa light chain variable region gene complex organization a  
 A:Reference number: N94689; M01D:88311394  
 A:Accession: C32513  
 A:Molecule type: DNA  
 A:Residues: 1-113 <KOF>  
 A:Cross-references: GB:M20830; NID:q196939; PIDN:AAA8844.1; PID:q196940  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 43.4%; Score 560; DB 2; Length 132;  
 Best Local Similarity 95.5%; Pred. No. 2.1e-33;  
 Matches 107; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 132 DVMTQTPPLTSLVITIGOPASISCKSSQSLSDSGKTYLNLQRPQSPKRLIYLVSKLD 191  
 DB 21 DVMTQTPPLTSLVITIGOPASISCKSSQSLSDSGKTYLNLQRPQSPKRLIYLVSKLD 80  
 QY 192 SGVPDRFTGSGSDFTLTKINRYEADLVGYVYCMOGTHSPLEAGTKLEI 243  
 DB 81 SGVPDRFTGSGSDFTLTKINRYEADLVGYVYCMOGTHSPLEAGTKLEI 132

## RESULT 5

F30560  
 Ig kappa chain V region (28.4.10A) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
 C:Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 21-Jan-2000  
 C:Accession: F30560  
 R:Matsuda, T.; Kabat, E.A.  
 J. Immunol. 142, 865-870, 1989  
 A:Title: Variable region cDNA sequences and antigen binding specificity of mouse mono  
 A:Reference number: A30560; M01D:89110062  
 A:Accession: F30560  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-113 <MAT>  
 A:Cross-references: GB:M24273; NID:q197081; PIDN:AAA63370.1; PID:q197082  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 42.9%; Score 553; DB 2; Length 113;  
 Best Local Similarity 94.6%; Pred. No. 5.5e-33;  
 Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 132 DVMTQTPPLTSLVITIGOPASISCKSSQSLSDSGKTYLNLQRPQSPKRLIYLVSKLD 191  
 DB 1 DVMTQTPPLTSLVITIGOPASISCKSSQSLSDSGKTYLNLQRPQSPKRLIYLVSKLD 60  
 QY 192 SGVPDRFTGSGSDFTLTKINRYEADLVGYVYCMOGTHSPLEAGTKLEI 243  
 DB 61 SGVPDRFTGSGSDFTLTKINRYEADLVGYVYCMOGTHSPLEAGTKLEI 112

## RESULT 6

S04576  
 Ig heavy chain precursor V region (MRL-h1stone 7H) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
 C:Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 21-Jan-2000  
 C:Accession: S04576  
 R:Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.;  
 Eur. J. Immunol. 17, 91-95, 1987  
 A:Title: Molecular analysis of the murine lupus-associated anti-self response: involv

A:Reference number: S04573; MUID:87133856  
 A:Accession: S04576  
 A:Molecule type: mRNA  
 A:Residues: 1-136 <KOP>  
 A:Cross-references: EMBL:X14624; NID:g52029; PIDN:CAA3277.1; PID:g52030  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C:Keywords: heterotrimer; Immunoglobulin  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>  
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 42.3%; Score 545.5; DB 2; Length 136;  
 Best Local Similarity 88.9%; Pred. No. 2,3e-32;  
 Matches 104; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVLOQSGAEIVRSGAVSLCTAGSFNKKDYMMWVKRPEQGLEWICWIDPENGDTLY 60  
 :|||||  
 Db 20 EVLOQSGAEIVRSGAVSLCTAGSFNKKDYMMWVKRPEQGLEWICWIDPENGDTLY 79  
 QY 61 ARFQKATMTDTSNTAYLQISLASDPAVYCNFYGD-ALDYWGQGTWTVSS 116  
 :|||||  
 Db 80 ASRFQKATMTDTSNTAYLQISLASDPAVYCNFYGD-ALDYWGQGTWTVSS 136

# RESULT 7

A55491  
 Proteolytic antibody light chain - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 21-Jan-2000  
 C:Accession: A55491  
 R:Gao, Q.S.; Sun, M.; Tyutyulkova, S.; Webster, D.; Rees, A.; Tramontano, A.; Massey, R.

J. Biol. Chem. 269, 32389-32393, 1994  
 A:Title: Molecular cloning of a proteolytic antibody light chain.  
 A:Reference number: A55491; MUID:95096089  
 A:Accession: A55491  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-112 <GAO>

A:Cross-references: GB:L34775  
 A:Note: authors translated the codon TAT for residue 37 as Thr  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 42.0%; Score 541; DB 2; Length 112;  
 Best Local Similarity 92.9%; Pred. No. 3,9e-32;  
 Matches 104; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 132 DVLMQTPPLTISVTIGOPASISCKSSQSLSDSGKTYLNMWLQRPQSPKRLIYVSKLD 191  
 :|||||  
 Db 1 DVMTQTPPLTISVTIGOPASISCKSSQSLSDSGKTYLNMWLQRPQSPKRLIYVSKLD 60

QY 192 SGVDPRTGSGSGTDFTLKINRVEADLGYYVCWQGTSPLEFGAGTKLEIK 243  
 :|||||  
 Db 61 SGVDPRTGSGSGTDFTLKINRVEADLGYYVCWQGTSPLEFGAGTKLEIK 112

# RESULT 8

A36259  
 Ig kappa chain V region (TE34) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 18-Jan-1991 #sequence\_revision 18-Jan-1991 #text\_change 21-Jan-2000  
 C:Accession: A36259  
 R:Zilber, B.; Scherf, T.; Levitt, M.; Anglistter, J.  
 Biochemistry 29, 10032-10041, 1990  
 A:Title: NMR-derived model for a peptide-antibody complex.  
 A:Reference number: A36259; MUID:91104915  
 A:Accession: A36259  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-112 <ZIL>

A:Cross-references: GB:M30458; GB:M30459; GB:M30480; GB:M30481; GB:M30482; GB:M30483

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C:Keywords: heterotrimer; Immunoglobulin  
 F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 41.8%; Score 539; DB 2; Length 112;  
 Best Local Similarity 92.9%; Pred. No. 5,4e-32;  
 Matches 104; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 132 DVLMQTPPLTISVTIGOPASISCKSSQSLSDSGKTYLNMWLQRPQSPKRLIYVSKLD 191  
 :|||||  
 Db 1 DVMTQTPPLTISVTIGOPASISCKSSQSLSDSGKTYLNMWLQRPQSPKRLIYVSKLD 60  
 QY 192 SGVDPRTGSGSGTDFTLKINRVEADLGYYVCWQGTSPLEFGAGTKLEIK 243  
 :|||||  
 Db 61 SGVDPRTGSGSGTDFTLKINRVEADLGYYVCWQGTSPLEFGAGTKLEIK 112

# RESULT 9

S20709  
 Ig kappa chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
 C:Accession: S20709  
 R:Brennan, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.;  
 submitted to the EMBL Data Library, April 1992  
 A:Description: Binding specificity and variable region sequences of two monoclonal an

A:Reference number: S20706  
 A:Accession: S20709  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-111 <BRE>  
 A:Cross-references: EMBL:Z11917; NID:g52655; PIDN:CAA77975.1; PID:g52656  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C:Keywords: heterotrimer; Immunoglobulin  
 F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 41.7%; Score 537; DB 2; Length 111;  
 Best Local Similarity 91.9%; Pred. No. 7,5e-32;  
 Matches 102; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 132 DVLMQTPPLTISVTIGOPASISCKSSQSLSDSGKTYLNMWLQRPQSPKRLIYVSKLD 191  
 :|||||  
 Db 1 DIQLOSPPLTISVTIGOPASISCKSSQSLSDSGKTYLNMWLQRPQSPKRLIYVSKLD 60

QY 192 SGVDPRTGSGSGTDFTLKINRVEADLGYYVCWQGTSPLEFGAGTKLEI 242  
 :|||||  
 Db 61 SGVDPRTGSGSGTDFTLKINRVEADLGYYVCWQGTSPLEFGAGTKLEI 111

# RESULT 10

S15672  
 Ig heavy chain V region - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
 C:Accession: S15672  
 R:Tempest, P.R.; Brenner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harri  
 Bio/Technology 9, 265-271, 1991  
 A:Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial  
 A:Reference number: S15672; MUID:91337412  
 A:Accession: S15672  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-116 <TEM>  
 A:Cross-references: EMBL:X58835; NID:g51978; PIDN:CAA1644.1; PID:g51979  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C:Keywords: heterotrimer; Immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 41.0%; Score 528; DB 2; Length 116;  
 Best Local Similarity 84.3%; Pred. No. 3,4e-31;

Matches	97; Conservative	7; Mismatches	11; Indels	0; Gaps	0;
QY	2	VOLQOOSGAELVRSGASVYKLTSCASTGENTKDYMMHWKORPEQGLEIMIPDENGDTGYA	61		
Db	2	VQLQXSGEILERSGASVYKLTSCASTGFNTKDYMMHWKORPEQGLEIMIPDENDVGYA	61		
QY	62	PKFGQKATMTADTSNSTAYLQLSLASDPTAVYCNFGDALDLYGQGTYYVSS	116		
Db	62	PKFGQKATMTADTSNSTAYLQLSLASDPTAVYCNFGSDGSDPDHMGQGTYYVSS	116		





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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 12, 2001, 15:23:24 ; Search time 16.14 Seconds  
(without alignments)  
486.212 Million cell updates/sec

Title: US-09-297-181-2  
Sequence: 1 QVQLQSGAEIVRSQASVYKL.....CWQGTSHPLTFGAGTKLEIK 243

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues  
Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	469	36.4	133	1 KV2F_HUMAN	P06310 homo sapien
2	428	33.2	113	1 KV2B_HUMAN	P01615 homo sapien
3	428	33.2	113	1 KV2D_HUMAN	P01617 homo sapien
4	428	33.2	113	1 KV2G_MOUSE	P01631 mus musculu
5	423	32.8	117	1 KV2E_HUMAN	P06309 homo sapien
6	423	32.8	139	1 HV07_MOUSE	P01751 mus musculu
7	418.5	32.5	115	1 KV2A_HUMAN	P01614 homo sapien
8	405.5	31.5	120	1 HV03_MOUSE	P01747 mus musculu
9	399	31.0	137	1 HV01_MOUSE	P01755 mus musculu
10	397.5	30.8	140	1 HV02_MOUSE	P01746 mus musculu
11	396.5	30.8	112	1 KV2C_HUMAN	P01756 mus musculu
12	384.5	29.8	113	1 HV12_MOUSE	P01744 homo sapien
13	384	29.8	113	1 HV1C_HUMAN	P01744 homo sapien
14	382	29.6	113	1 KV2C_MOUSE	P01628 mus musculu
15	382	29.6	113	1 KV2F_MOUSE	P01630 mus musculu
16	380.5	29.5	117	1 HV13_MOUSE	P01757 mus musculu
17	380	29.5	118	1 HV51_MOUSE	P06330 mus musculu
18	378	29.3	112	1 KV2A_MOUSE	P01626 mus musculu
19	377	29.2	113	1 KV2E_MOUSE	P03916 mus musculu
20	377	29.2	120	1 HV50_MOUSE	P06329 mus musculu
21	375.5	29.1	138	1 HV48_MOUSE	P03980 mus musculu
22	372.5	28.9	111	1 KV3N_MOUSE	P01759 mus musculu
23	372.5	28.9	136	1 HV15_MOUSE	P01666 mus musculu
24	371	28.8	112	1 KV2D_MOUSE	P01629 mus musculu
25	367.5	28.5	111	1 KV3M_MOUSE	P01665 mus musculu
26	367.5	28.5	121	1 HV3K_MOUSE	P01745 mus musculu
27	365.5	28.4	108	1 KVI1_CANFA	P01667 mus musculu
28	365.5	28.4	111	1 KV3O_MOUSE	P01667 mus musculu
29	364	28.2	117	1 HV09_MOUSE	P01753 mus musculu
30	363.5	28.2	111	1 KV3J_MOUSE	P01664 mus musculu
31	360.5	28.0	111	1 KV3Q_MOUSE	P01669 mus musculu
32	359	27.9	110	1 KV3P_MOUSE	P01668 mus musculu
33	358.5	27.8	134	1 KV4C_HUMAN	P06314 homo sapien

34	358	27.8	117	1 HV06_MOUSE	P01750 mus musculu
35	352	27.3	117	1 HV04_MOUSE	P01748 mus musculu
36	352	27.3	117	1 HV49_MOUSE	P06328 mus musculu
37	351	27.2	117	1 HV1B_HUMAN	P01743 homo sapien
38	350.5	27.2	111	1 KV3U_MOUSE	P01673 mus musculu
39	350.5	27.2	114	1 KV4A_HUMAN	P01625 homo sapien
40	349.5	27.1	111	1 KV3K_MOUSE	P01671 mus musculu
41	348.5	27.0	111	1 KV3S_MOUSE	P01671 mus musculu
42	348	27.0	117	1 HV10_MOUSE	P01754 mus musculu
43	348	27.0	117	1 HV52_MOUSE	P06327 mus musculu
44	347.5	27.0	111	1 KV3H_MOUSE	P01660 mus musculu
45	345.5	26.8	131	1 KV3I_MOUSE	P01661 mus musculu

## ALIGNMENTS

RESULT	ID	Sequence	STANDARD	PRT	AA
1	KV2F_HUMAN	P06310		133	AA
AC	P06310				
DT	01-JAN-1988	(Rel. 06, last sequence update)			
DT	01-JAN-1988	(Rel. 06, last sequence update)			
DT	15-JUL-1999	(Rel. 38, last annotation update)			
DE	IG KAPPA CHAIN V-II REGION RPMI 6410 PRECURSOR				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-86041852; PubMed-2997711;				
RA	Klobeck H.G., Meisel A., Combratio G., Solomon A., Zachau H.G.;				
RT	"Human immunoglobulin kappa light chain genes of subgroups II and III."				
RL	Nucleic Acids Res. 13:6499-6513(1985).				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	the European Bioinformatics Institute. There are no restrictions on its				
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CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>				
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).				
CC	-----				
DR	EMBL: Z00020; CAA77315.1; -				
DR	PIR: A01890; K2HURP.				
DR	INTERPRO: IPR003006; -				
DR	PFAM: PF00047; 19; 1.				
KW	Immunoglobulin V region; Signal.				
FT	SIGNAL	1	20		
FT	CHAIN	21	133		IG KAPPA CHAIN V-II REGION RPMI 6410.
FT	DOMAIN	21	43		FRAMEWORK 1.
FT	DOMAIN	44	59		COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN	60	74		FRAMEWORK 2.
FT	DOMAIN	75	81		COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN	82	113		FRAMEWORK 3.
FT	DOMAIN	114	122		COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN	123	132		FRAMEWORK 4.
FT	DISULFID	43	113		BY SIMILARITY.
FT	NON_TER	133	133		
SQ	SEQUENCE	133	AA; 14707	MM; 5130	CAR3673009EE CRC64;

Query Match 36.4%; Score 469; DB 1; Length 133;

Best Local Similarity 76.7%; Pred. No. 2.5e-29;

Matches 89; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

128 GGSGLVMDQPTLTITVIGOPASISCKSSOSLDSDGTYLWLLRGOSPKRLITLV 187

17 GSSGDMVMDQSPISLPTVITIGOPASISCKSSOSLYVSDGTYLWLLRGOSPKRLITLV 76

188 SKLDSGVPRFTGSGSGDTFTLKINRVEADLGVYCMQGTSHPLTFGAGTKLEIK 243

Db 77 SNRSGVDPFRSGSGDTFTLKISRVEADGVYVCMQGTHTMSWTGGTKVEIK 132

RESULT 2

KV2B\_HUMAN STANDARD; PRT; 113 AA.

ID KV2B\_HUMAN

AC P01615;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-II REGION FR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

RN [1]

RP SEQUENCE.

RX MEDLINE-76253627; PubMed-821524;

RA Riesen W.F., Jaton J.C.;

RT "Variable region sequence of the light chain from a Waldenstroms IgM with specificity for phosphorylcholine.";

RL Biochemistry 15:3829-3833(1976).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.

DR PIR; A01886; K2HUTR.

DR INTERPRO; IPR003006; -.

KM Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK 1.

FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 40 54 FRAMEWORK 2.

FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 62 93 FRAMEWORK 3.

FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 103 112 FRAMEWORK 4.

FT DISULFID 23 93 BY SIMILARITY.

FT NON\_TER 113 113

SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match 33.2%; Score 428; DB 1; Length 113;

Best Local Similarity 71.4%; Pred. No. 2,7e-26;

Matches 80; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 132 DVMTQPTPLTSLVITIGOPASISCKSSQSLSDSGKTYLMLLQRPQSPKRLIYLVSRLD 191

Db 1 DVMTQSPFLPTVLGPASISCKSSQSLVYRBGTYLBMYLQKPGQPELLIYLSYRD 60

QY 192 SGVPDRFTSGSGSDTFTLKISRVEADGVYVCMQGTHTMSWTGGTKVEIK 243

Db 61 SGVPDRFTSGSGSDTFTLKISRVEADGVYVCMQGTHTMSWTGGTKVEIK 112

RESULT 3

KV2D\_HUMAN STANDARD; PRT; 113 AA.

ID KV2D\_HUMAN

AC P01617;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-II REGION TEM.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

RN [1]

RP SEQUENCE (BENCE-JONES PROTEIN TEM).

RX MEDLINE-7418480; PubMed-4596148;

RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;

RT "Amino acid sequence of a kappa Bence Jones protein from a case of primary amyloidosis.";

RL Biochemistry 12:3763-3780(1973).

RN [2]

RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEM).

RX MEDLINE-73166538; PubMed-4700495;

RA Terry W.D., Page D.L., Kimura S., Isobe T., Osseman E.F.,

RA Glenner G.G.;

RT "Structural identity of Bence Jones and amyloid fibril proteins in a patient with plasma cell dyscrasia and amyloidosis.";

RL J. Clin. Invest. 52:1276-1281(1973).

CC -1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.

CC -1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A PATIENT WITH PLASMA CELL DYSKRASIA AND AMYLOIDOSIS.

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.

DR PIR; A01886; K2HUTR.

DR INTERPRO; IPR003006; -.

KM Immunoglobulin V region; Bence-Jones protein; Amyloid.

FT DOMAIN 1 23 FRAMEWORK 1.

FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 40 54 FRAMEWORK 2.

FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 62 93 FRAMEWORK 3.

FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 103 112 FRAMEWORK 4.

FT DISULFID 23 93 BY SIMILARITY.

FT NON\_TER 113 113

SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query Match 33.2%; Score 428; DB 1; Length 113;

Best Local Similarity 71.4%; Pred. No. 2,7e-26;

Matches 80; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 132 DVMTQPTPLTSLVITIGOPASISCKSSQSLSDSGKTYLMLLQRPQSPKRLIYLVSRLD 191

Db 1 DVMTQSPFLPTVLGPASISCKSSQSLVYRBGTYLBMYLQKPGQPELLIYLSYRD 60

QY 192 SGVPDRFTSGSGSDTFTLKISRVEADGVYVCMQGTHTMSWTGGTKVEIK 243

Db 61 SGVPDRFTSGSGSDTFTLKISRVEADGVYVCMQGTHTMSWTGGTKVEIK 112

RESULT 4

KV2G\_MOUSE STANDARD; PRT; 113 AA.

ID KV2G\_MOUSE

AC P01631;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-II REGION 26-10.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE.

RC STRAIN-A/J;

RX MEDLINE-83178921; PubMed-6404298;

RA Novotny J., Margolies M.N.;

RT "Amino acid sequence of the light chain variable region from a mouse anti-dioxin hybridoma antibody.";

RL Biochemistry 22:1153-1158(1983).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA PROTEIN THAT BINDS DIOXIN.

CC PIR; A01914; KMS26.

DR INTERPRO; IPR003006; -.

KM Immunoglobulin V region; Monoclonal antibody; Hybridoma.

FT DOMAIN 1 23 FRAMEWORK 1.

FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 40 54 FRAMEWORK 2.

FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 62 93 FRAMEWORK 3.

FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 103 112 FRAMEWORK 4.

FT DISULFID 23 93 BY SIMILARITY.



DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-II REGION CUM.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE-68242259; PubMed-5586923;  
 RA Hilschmann N.;  
 RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-  
 type)." ;  
 RL Hope-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).  
 RN [2]  
 RP REVISIONS TO 50; 52; 96 AND 97.  
 RX MEDLINE-70063440; PubMed-4188189;  
 RA Hilschmann N.;  
 RT "Molecular basis of antibody formation." ;  
 RL Naturwissenschaften 56:195-205(1969).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 DE IG HEAVY CHAIN V REGION S43 PRECURSOR.  
 DR PIR: A01885; K2HUCM.  
 DR INTERPRO: IPR003006; .  
 KW PFAM: PF00047; 15; 1.  
 KM Immunoglobulin V region; Bence-Jones protein.  
 FT DISULFID 24 95  
 FT NON\_TER 115 115 BY SIMILARITY.  
 SO SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 32.5%; Score 418.5; DB 1; Length 115;  
 Best Local Similarity 72.6%; Pred. No. 1.5e-25;  
 Matches 82; Conservative 13; Mismatches 17; Indels 1; Gaps 1;

QY 132 DVLNQTPLTSLTIGQPSISCKSSQSLDS-DGKTYLNTMLRGQSPKRLIYVSKL 190  
 DB 2 DVLNQTPLTSLTIGQPSISCKSSQSLDS-DGKTYLNTMLRGQSPKRLIYVSKL 61  
 QY 191 DSGVPRFTSGSGDTFTLKINFEAEADLGYYCMQGTSPITFGAGTKLEIK 243  
 DB 62 ASGVPRFTSGSGDTFTLKINFEAEADLGYYCMQGTSPITFGAGTKLEIK 114

RESULT 8  
 ID HV03\_MOUSE STANDARD; PRT; 120 AA.  
 AC P01747;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V REGION 36-65.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-8313846; PubMed-6186498;  
 RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,  
 RA Marshak-Rothstein A.;  
 RT "The genetic basis of antibody production: the dominant anti-arsenate  
 idotype response of the strain A mouse." ;  
 RL Eur. J. Immunol. 12:1023-1032(1982).  
 CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER  
 DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS  
 CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J  
 SEGMENT, JH2.  
 CC PIR: A02028; HVM5G7.  
 DR INTERPRO: IPR003006; .  
 DR PFAM: PF00047; 15; 1.  
 KM Immunoglobulin V region; Antiarsonate antibody; Hybridoma.  
 FT NON\_TER 120 120  
 SO SEQUENCE 120 AA; 13307 MW; F04E4A167B54AF CRC64;

Query Match 31.5%; Score 405.5; DB 1; Length 120;  
 Best Local Similarity 65.0%; Pred. No. 1.5e-24;  
 Matches 78; Conservative 18; Mismatches 19; Indels 5; Gaps 2;

QY 2 VOLQOSGAELVRSASVKSCTASGFNIKDYMHVKRPEGLGKIDPENGDTXA 61  
 DB 1 VOLQOSGAELVRSASVKSCTASGFNIKDYMHVKRPEGLGKIDPENGDTXA 60  
 QY 62 PKFGKATMTADTSSNTATLQSLASEDTAYVYCN---FYGDA--LDVWGQGTIVYSS 116  
 DB 61 EKFKGKTTLVDKSSSTAYVQRLSLTSEDSAYVFCARSVYGGSTYFDVWGQGTITVSS 120

RESULT 9  
 ID HV11\_MOUSE STANDARD; PRT; 137 AA.  
 AC P01755;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V REGION S43 PRECURSOR.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-81234548; PubMed-6788376;  
 RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajesky K.,  
 RA Baltimore D.;  
 RT "Heavy chain variable region contribution to the NPB family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region." ;  
 RL Cell 24:625-637(1981).  
 CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA  
 MAKING ANTIBODIES TO THE HAPPEN (4-HYDROXY-3-NITROPHENYL)ACETYL  
 (NPB ANTIBODIES).  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: J00539; AAA38172.1; .  
 DR PIR: A02038; G2MS43.  
 DR INTERPRO: IPR003006; .  
 DR PFAM: PF00047; 15; 1.  
 KM Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.  
 FT DOMAIN 20 49 FRAMEWORK 1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 55 68 FRAMEWORK 2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 86 117 FRAMEWORK 3.  
 FT DOMAIN 118 122 D SEGMENT.  
 FT DOMAIN 123 137 JH2 SEGMENT.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON\_TER 137 137  
 SO SEQUENCE 137 AA; ADD5881BF44B8EC9 CRC64;

Query Match 31.0%; Score 399; DB 1; Length 137;  
 Best Local Similarity 66.1%; Pred. No. 5.3e-24;  
 Matches 78; Conservative 10; Mismatches 28; Indels 2; Gaps 1;

QY 1 VOLQOSGAELVRSASVKSCTASGFNIKDYMHVKRPEGLGKIDPENGDTXA 60  
 DB 20 VOLQOSGAELVRSASVKSCTASGFNIKDYMHVKRPEGLGKIDPENGDTXA 79  
 QY 61 AKFGKATMTADTSSNTATLQSLASEDTAYVYCNFY--GDALDYWGQGTIVYSS 116

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RP SEQUENCE.
RA Dreyer W.J., Gray M.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
RT some facts and a unifying hypothesis.";
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.
DR PIR: A01887; K2HMUL.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 53 FRAMEWORK 2.
FT DOMAIN 4 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 61 FRAMEWORK 3.
FT DOMAIN 6 92 FRAMEWORK 4.
FT DOMAIN 7 101 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 102 111 FRAMEWORK 4.
FT NON_TER 23 92 BY SIMILARITY.
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ADE481 CRC64;

Query Match 30.8%; Score 396.5; DB 1; Length 112;
Best Local Similarity 63.4%; Pred. No. 6.6e-24;
Matches 71; Conservative 25; Mismatches 15; Indels 1; Gaps 1

QY 132 DVLMTQPTLTSTYITIGOPASISCKSSQSLSDSGKTYLNMLLRPGSPRLTYLVSKL D 191
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1 DVLQSPSLPTPTPEEPASISCRSSQNLDSBGR-YLDWTLZLRPGASPLZLLYIGSNRA 59
QY 192 SGVPRDFRSGSGSDFTLTKINRVEADIGVYICWQGHSPLTFAAGKLEIK 243
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 60 SGVPRDFRSGSGSDFTLTKISRVAZABGVYICWQALQPTLTFGCGTNVEIK 111

RESULT 12
HV12_MOUSE STANDARD; PRT; 117 AA.
ID HV12_MOUSE
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 104E.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RX MEDLINE:83075343; PubMed:6816276;
RA Kehry M.R., Fuhman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5444(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR: A02039; M4MSAE.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region; glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 29.8%; Score 384.5; DB 1; Length 117;
Best Local Similarity 65.0%; Pred. No. 5.6e-23;
Matches 76; Conservative 12; Mismatches 28; Indels 1; Gaps 1

1 QVQLQSGAEIVYSGASVKLTCTASGFKNIKYYMHVYKQRPEDGLIEWIGWDENGDTEY 60

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Db 1 EVOLQOOSGPELVKRGASVKKMSCKASGYTFIDYMKWVKOSHGKSLIEWIGINPNNGSTSY 60  
 QY 61 APPFOGATMTADTSSNTATVLOLSLASEPTAYVC-NFGDMLADYGOGTIVVSS 116  
 Db 61 NQFKGATLTVDSKSSSTAYMQLNLSISEDAVYCAKRDYDFWAGGTIVVSS 117

RESULT 13  
 HYLIC\_HUMAN STANDARD; PRT; 143 AA.  
 AC P01744;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V-I REGION ND PRECURSOR (FRAGMENTS).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83065234; PubMed=6815656;  
 RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,  
 Bell L.O., Gould H.J.,  
 RT "Cloning and sequence determination of the gene for the human  
 RT immunoglobulin epsilon chain expressed in a myeloma cell line."  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).  
 RN [2]  
 RP SEQUENCE OF 16-142.  
 RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;  
 RL (in) Bach M.K. (eds.);  
 RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,  
 RL Marcel Dekker, New York (1978).  
 CC -1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA  
 CC PROTEIN.  
 DR PIR; A02026; EIHUND.  
 DR PFAM; PF00047; 19; 1.  
 KW Immunoglobulin V region; Signal.  
 FT NON\_CONS 4 5  
 FT SGNL 1 15  
 FT CHAIN 16 143 IG HEAVY CHAIN V-I REGION ND.  
 FT MOD\_RES 16 16 PYROLIDONE CARBOXYLIC ACID.  
 FT DISULFID 37 111  
 FT CONFLICT 17 17 T -> V (IN REF. 2).  
 FT CONFLICT 49 50 IH -> HI (IN REF. 2).  
 FT CONFLICT 63 64 VG -> GV (IN REF. 2).  
 FT CONFLICT 121 121 MISSING (IN REF. 2).  
 FT NON\_TER 143 143  
 SQ SEQUENCE 143 AA; 16051 MW; DE80DD280D002027E CRC64;

Query Match 29.8%; Score 384; DB 1; Length 143;  
 Best Local Similarity 56.2%; Pred. No. 7.7e-23;  
 Matches 72; Conservative 18; Mismatches 26; Indels 12; Gaps 2;

QY 1 QVQLQSGALVSGASVYKLSCTASGFINIKDYMMWVKORPEQGLEWIGMIDPENGDTPEY 60  
 Db 16 QTVLQSGALVSGASVYKLSCTASGFINIKDYMMWVKORPEQGLEWIGMIDPENGDTPEY 75  
 QY 61 APPFOGATMTADTSSNTATVLOLSLASEPTAYVC-----NF-YGDALDYWCQ 108  
 Db 76 APPFOGATMTADTSSNTATVLOLSLASEPTAYVC-----NF-YGDALDYWCQ 135  
 QY 109 GTTVTVSS 116  
 Db 136 GTTVTVSS 143

RESULT 14  
 KY2C\_MOUSE STANDARD; PRT; 113 AA.  
 AC P01628;  
 DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-II REGION MOPC 511.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=81052016; PubMed=6776396;  
 RA Appella E.;  
 RT "Amino acid sequence of the light chain variable region of M511, a  
 RT phosphoricholine-binding murine myeloma protein."  
 RL Mol. Immunol. 17:711-718(1980).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 CC BINDS PHOSPHORYLCHOLINE.  
 DR PIR; A01910; KYMS51.  
 DR INTERPRO; IPR003006; -  
 DR PFAM; PF00047; 19; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 39 FRAMEWORK 2.  
 FT DOMAIN 40 54 FRAMEWORK 3.  
 FT DOMAIN 55 61 FRAMEWORK 4.  
 FT DOMAIN 62 93 FRAMEWORK 5.  
 FT DOMAIN 94 102 FRAMEWORK 6.  
 FT DOMAIN 103 112 FRAMEWORK 7.  
 FT DISULFID 23 93 BY SIMILARITY.  
 FT NON\_TER 113 113  
 SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;

Query Match 29.6%; Score 382; DB 1; Length 113;  
 Best Local Similarity 67.0%; Pred. No. 8.4e-23;  
 Matches 75; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

QY 132 DVLTQTPPLTISTIQPASIISCKSSQSLSDSGKTYLNLQRPQSPKRLTYLSKLD 191  
 Db 1 DIYTDDELSPYTSGBSEVISISCRSSKSLYKDGKTYLWFLQGPQSPPLTYLWSTRA 60  
 QY 192 SGVSDPFTSGSGTDFTLKINREAVDLGYVYCWGTHSPFLFGAGTKLEIK 243  
 Db 61 SGVSDPFTSGSGTDFTLKINREAVDLGYVYCWGTHSPFLFGAGTKLEIK 112

RESULT 15  
 KY2E\_MOUSE STANDARD; PRT; 113 AA.  
 AC P01630;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DE IG KAPPA CHAIN V-II REGION 7S34.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=83256427; PubMed=6409088;  
 RA Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;  
 RT "A new isotype sequence (V kappa 27) of the variable region of kappa-  
 RT light chains from a mouse hybridoma-derived anti-(streptococcal group  
 RT A polysaccharide) antibody containing an additional cysteine residue.  
 RT Application of the dimethylaminoozobenzene isothiocyanate technique  
 RT for the isolation of peptides."  
 RL Biochem. J. 211:173-180(1983).  
 CC -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL  
 CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.  
 DR PIR; A01913; KYMS7S.  
 DR INTERPRO; IPR003006; -  
 DR PFAM; PF00047; 19; 1.  
 KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.



FT DOMAIN 40 54 FRAMEWORK 2.  
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 62 93 FRAMEWORK 3.  
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 103 112 FRAMEWORK 4.  
FT DISULFID 23 93 BY SIMILARITY.  
FT NON\_TER 113 113  
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 29.68; Score 382; DB 1; Length 113;  
Best Local Similarity 67.0%; Pred. No. 8.4e-23;  
Matches 75; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

OY 132 DVLMTOTPLFLSYTIGOPASISCKSSQSLDSOGKTYLNLORPGOSPRLIYLYSKLD 191  
DB 1 DIVMTQTAPSAALYTPGESVSISCRSSKSLHNSGNTLYLNFLORPQCCPOLLIYRMSNLA 60  
OY 192 SGVPDRFTSGSGSGTDFTLKINRYEAEDLGYYCWCQGTSPITFGAGTKLEIK 243  
DB 61 SGVPDRFTSGSGSGTAFPLRISRYEAEDVGYYCWCQGTSPITFGAGTKLEIK 112

Search completed: February 12, 2001, 15:26:39  
Job time: 195 sec

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OM protein - protein search, using sw model

Run on: February 12, 2001, 15:22:50 ; Search time 42.85 seconds  
(without alignments)  
664,680 Million cell updates/sec

Title: US-09-297-181-2  
Perfect score: 1289  
Sequence: 1 QVQLQSGAEIVRSQASVYK.....CMQGHSPLEPFAGTKLEIK 243

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues  
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP.TREMBL\_15:\*  
2: SP.Archea:\*  
3: SP.Bacteria:\*  
4: SP.Fungi:\*  
5: SP.Human:\*  
6: SP.Invertebrate:\*  
7: SP.Mammal:\*  
8: SP.Mhc:\*  
9: SP.Organelle:\*  
10: SP.Phage:\*  
11: SP.Plant:\*  
12: SP.Protozoa:\*  
13: SP.Virus:\*  
14: SP.Vertebate:\*  
15: SP.Unclassified:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	696.5	54.0	298	11 Q9YF0	Q9YF0 mus musculi
2	447.5	34.7	114	4 Q9UL80	Q9UL80 homo sapien
3	443.5	34.4	109	11 Q9UL85	Q9UL85 mus musculi
4	428	33.2	118	11 Q9ULC4	Q9ULC4 mus musculi
5	401.5	31.1	117	11 Q9QX9	Q9QX9 mus musculi
6	396.5	30.8	117	11 Q9QXFO	Q9QXFO mus musculi
7	393.5	30.5	125	4 Q9UL95	Q9UL95 mus musculi
8	393	30.5	104	11 Q9UL82	Q9UL82 mus musculi
9	390	30.3	124	4 Q9UL92	Q9UL92 mus musculi
10	385.5	29.9	119	4 Q9UL94	Q9UL94 mus musculi
11	384	29.8	114	11 Q9UL81	Q9UL81 mus musculi
12	381	29.6	109	11 Q9UL75	Q9UL75 mus musculi
13	372	28.9	110	11 Q9UL77	Q9UL77 mus musculi
14	367.5	28.5	150	4 Q9Y298	Q9Y298 mus musculi
15	354.5	27.5	117	11 Q9ULC6	Q9ULC6 mus musculi
16	332	25.8	110	11 Q9UL83	Q9UL83 mus musculi
17	330.5	25.6	157	4 Q9S978	Q9S978 mus musculi
18	326	25.3	109	4 Q9UL78	Q9UL78 mus musculi
19	320	24.8	116	4 Q9UL89	Q9UL89 mus musculi

20	317.5	24.6	113	4 Q9UL90	Q9UL90 mus musculi
21	311	24.1	107	4 Q9UL81	Q9UL81 mus musculi
22	310.5	24.1	121	4 Q9UL71	Q9UL71 mus musculi
23	309.5	24.0	108	4 Q9UL77	Q9UL77 mus musculi
24	309.5	24.0	116	4 Q9UL93	Q9UL93 mus musculi
25	305.5	23.7	108	4 Q9UL70	Q9UL70 mus musculi
26	305.5	23.5	131	4 Q9UL88	Q9UL88 mus musculi
27	302.5	23.4	147	4 Q9Y509	Q9Y509 mus musculi
28	301	23.4	109	4 Q9UL86	Q9UL86 mus musculi
29	298	23.1	109	4 Q9UL72	Q9UL72 mus musculi
30	297	23.0	118	4 Q9UL79	Q9UL79 mus musculi
31	296.5	22.8	118	4 Q9UL91	Q9UL91 mus musculi
32	294	22.8	118	4 Q9UL84	Q9UL84 mus musculi
33	293	22.7	106	5 Q9UL10	Q9UL10 mus musculi
34	292	22.7	106	5 Q9UL80	Q9UL80 mus musculi
35	291	22.6	124	6 Q9UL79	Q9UL79 mus musculi
36	289.5	22.5	102	11 Q9UL80	Q9UL80 mus musculi
37	289.5	22.5	103	11 Q9UL80	Q9UL80 mus musculi
38	289.5	22.5	108	4 Q9UL83	Q9UL83 mus musculi
39	289	22.4	124	6 Q9UL84	Q9UL84 mus musculi
40	288	22.3	150	4 Q9S973	Q9S973 mus musculi
41	286.5	22.2	119	4 Q9UL73	Q9UL73 mus musculi
42	285	22.1	109	4 Q9UL85	Q9UL85 mus musculi
43	282.5	21.9	99	11 Q9UL74	Q9UL74 mus musculi
44	274	21.3	437	11 Q9UL14	Q9UL14 mus musculi
45	268.5	20.8	104	4 Q9UL87	Q9UL87 mus musculi

## ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	298 AA.
Q9YF0	Q9YF0			
AC	Q9YF0			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	CN 8 SCFV.			
GN	CN 8.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_Taxid:10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BALB/C; ISSUE-SPLEEN;			
RA	Shiohara N., Demura T., Fukuda H.;			
RT	Isolation of a novel type of vascular cell wall-specific monoclonal			
RT	antibody recognizing a cell polarity using a phase display subtraction			
RT	method.			
RL	Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AB036341; BAA86633.1; -			
DR	HSSP: P01607; IREL.			
DR	INTERPRO: IPR003006; -			
DR	PFAM: PF00047; Ig; 2.			
DR	SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;			

Query Match 54.0%; Score 696.5; DB 11; Length 298;  
Best Local Similarity 53.3%; Pred. No. 2.9e-54;  
Matches 131; Conservative 43; Mismatches 63; Indels 9; Gaps 3;

QY	1 QVQLQSGAEIVRSQASVYK.....CMQGHSPLEPFAGTKLEIK 243
DB	40 QVQLQSGGCVKPGGSLKSCAASGDFSRVMSVWVRPGGELWELINDSTINY 99
QY	61 APTFOCKATMTADTSNTAYVLOLSIASSEDYAVYVC---NFYGDALDYGCGTAVVSSG 117



```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225174; CAB65237.1;
DR INTERPRO; IPR003006;
DR PFAM; PF00047; 19; 1.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D9734 CRC64;

Query Match 31.1%; Score 401.5; DB 11; Length 117;
Best Local Similarity 65.5%; Pred. No. 1.5e-28;
Matches 78; Conservative 15; Mismatches 21; Indels 5; Gaps 2;

OY 1 OV0LOSGAEIVSGASVRLCTAGSFNIKDYMHVKORPEGLEWIGWIDPENGDTXY 60
   :||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1 EV0LOSGPELVKPGASVSKASGTFYDYMKWKOSHGSLEWIGDINPNSGTY 60
   :||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

OY 61 APRFGKATMTADTSSNTAYLQSLASEDTAYYC--NFYGDALDYWGQTTVYSS 116
   :||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 61 NQFKGKATLTVDKSSSTAYMQLNSTSEDSAYYCCARDRY--AMDYWGQTSVYSS 117
   :||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 6
O9QXFO PRELIMINARY; PRT; 117 AA.
AC O9QXFO;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225171; CAB65236.1;
DR INTERPRO; IPR003006;
DR PFAM; PF00047; 19; 1.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 30.8%; Score 396.5; DB 11; Length 117;
Best Local Similarity 64.2%; Pred. No. 4.3e-28;
Matches 77; Conservative 15; Mismatches 21; Indels 7; Gaps 2;

OY 1 OV0LOSGAEIVSGASVRLCTAGSFNIKDYMHVKORPEGLEWIGWIDPENGDTXY 60
   :||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1 EV0LOSGPELVKPGASVSKASGTFYDYMKWKOSHGSLEWIGDINPNSGTY 60
   :||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

OY 61 APRFGKATMTADTSSNTAYLQSLASEDTAYYC--NFYGDALDYWGQTTVYSS 116
   :||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 61 NQFKGKATLTVDKSSSTAYMQLNSTSEDSAYYCCARDRY--FDYWGQTTLVSS 117
   :||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 7
O9UL95 PRELIMINARY; PRT; 125 AA.
AC O9UL95;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).

```

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
DE "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035019; AAD56255.1;
DR INTERPRO; IPR003006;
DR PFAM; PF00047; 19; 1.
FT NON_TER 1 1
FT NON_TER 125 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 30.5%; Score 393.5; DB 4; Length 125;
Best Local Similarity 59.2%; Pred. No. 8.7e-28;
Matches 74; Conservative 16; Mismatches 26; Indels 9; Gaps 1;

OY 1 OV0LOSGAEIVSGASVRLCTAGSFNIKDYMHVKORPEGLEWIGWIDPENGDTXY 60
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1 EV0LVSGAEVKKPGASVSKASGTYTGYMHVKORPEGLEWIGWIDPENGDTXY 60
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

OY 61 APRFGKATMTADTSSNTAYLQSLASEDTAYYC-----NFYGDALDYWGQTT 111
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 61 AQRVGRVMTMDTITSTAYMELSRISDPTAVYCCARSQGGRIAAAGDADWIGQTM 120
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

OY 112 VTYSS 116
Db 121 VTYSS 125

RESULT 8
O9JL82 PRELIMINARY; PRT; 104 AA.
AC O9JL82;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Walker S., Liang L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RL acetylglucosamine antibodies from mice with autoimmune myocarditis."
DR EMBL; AF206024; AAF69322.1;
FT NON_TER 1 1
FT NON_TER 104 104
SQ SEQUENCE 104 AA; 11360 MW; 5DA8B8F5F0AA1AE CRC64;

Query Match 30.5%; Score 393; DB 11; Length 104;
Best Local Similarity 73.1%; Pred. No. 7.6e-28;
Matches 76; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

OY 140 JLTVYIGIPASISCKSSQSLDSGKTYLNLQRPQSPRLIYVSKLDSGYDPRT 199
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1 LSLPVLSDGQASISCKSSQSLVHTNNTLYLHWYLOKPGSPILLITKYNSRSGVPDRS 60
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

OY 200 GSGSGDFTLKINRAEDLGYVYCCQGHSPLTGAGTKLEIK 243
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 61 GSGSGDFTLKISRVAEDLGYVYCCQGHSPLTGAGTKLEIK 104
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

```









GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2001, 15:22:45 ; Search time 28.25 seconds

(without alignments)  
294.127 Million cell updates/sec

Title: US-09-297-181-2

Perfect score: 1289

Sequence: 1 QVQLQSGAEIVRSASVKL.....CMQGTSHPLTFGATKLEIK 243

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
A.Geneseq\_36:\*  
1: /SIDSL/gcgdata/geneseq/geneseqp/AA1980.DAT:\*  
2: /SIDSL/gcgdata/geneseq/geneseqp/AA1981.DAT:\*  
3: /SIDSL/gcgdata/geneseq/geneseqp/AA1982.DAT:\*  
4: /SIDSL/gcgdata/geneseq/geneseqp/AA1983.DAT:\*  
5: /SIDSL/gcgdata/geneseq/geneseqp/AA1984.DAT:\*  
6: /SIDSL/gcgdata/geneseq/geneseqp/AA1985.DAT:\*  
7: /SIDSL/gcgdata/geneseq/geneseqp/AA1986.DAT:\*  
8: /SIDSL/gcgdata/geneseq/geneseqp/AA1987.DAT:\*  
9: /SIDSL/gcgdata/geneseq/geneseqp/AA1988.DAT:\*  
10: /SIDSL/gcgdata/geneseq/geneseqp/AA1989.DAT:\*  
11: /SIDSL/gcgdata/geneseq/geneseqp/AA1990.DAT:\*  
12: /SIDSL/gcgdata/geneseq/geneseqp/AA1991.DAT:\*  
13: /SIDSL/gcgdata/geneseq/geneseqp/AA1992.DAT:\*  
14: /SIDSL/gcgdata/geneseq/geneseqp/AA1993.DAT:\*  
15: /SIDSL/gcgdata/geneseq/geneseqp/AA1994.DAT:\*  
16: /SIDSL/gcgdata/geneseq/geneseqp/AA1995.DAT:\*  
17: /SIDSL/gcgdata/geneseq/geneseqp/AA1996.DAT:\*  
18: /SIDSL/gcgdata/geneseq/geneseqp/AA1997.DAT:\*  
19: /SIDSL/gcgdata/geneseq/geneseqp/AA1998.DAT:\*  
20: /SIDSL/gcgdata/geneseq/geneseqp/AA1999.DAT:\*  
21: /SIDSL/gcgdata/geneseq/geneseqp/AA2000.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1289	100.0	243	19	W60769 Single chain antib
2	1277	99.1	535	18	W28491 Human p53 protein
3	1277	99.1	535	18	W28492 Human p53 protein
4	983.5	76.5	353	20	Y6273 Anti Fc alpha rece
5	961	74.6	249	19	W60770 Single chain antib
6	911	70.7	281	20	W82744 Fusion protein PIC
7	911	70.7	281	20	W82745 Fusion protein (80
8	906	70.3	270	16	R75719 MPE-23 antibody
9	900	69.8	553	18	W15508 Single chain anti-
10	900	69.8	553	18	W15508 Single chain anti-
11	895.5	69.5	249	9	P80154 H22-anti-CEA antib
12	886.5	68.8	437	19	W37738 Nucleotide sequenc

13	869	67.4	532	21	Y78328	Bispecific anti-ze
14	866	67.2 <td>348</td> <td>20</td> <td>Y29910 <td>Human IP-10 and mu</td> </td>	348	20	Y29910 <td>Human IP-10 and mu</td>	Human IP-10 and mu
15	866	67.2 <td>361</td> <td>20</td> <td>Y29912 <td>Human MCP-3 and mu</td> </td>	361	20	Y29912 <td>Human MCP-3 and mu</td>	Human MCP-3 and mu
16	863	67.0 <td>251</td> <td>20</td> <td>Y17958 <td>Mouse scFv fragmen</td> </td>	251	20	Y17958 <td>Mouse scFv fragmen</td>	Mouse scFv fragmen
17	859	66.6 <td>251</td> <td>20</td> <td>Y17962 <td>Mouse scFv fragmen</td> </td>	251	20	Y17962 <td>Mouse scFv fragmen</td>	Mouse scFv fragmen
18	856.5	66.4 <td>311</td> <td>11</td> <td>R05378 <td>Multi-functional pr</td> </td>	311	11	R05378 <td>Multi-functional pr</td>	Multi-functional pr
19	850	65.9 <td>242</td> <td>20</td> <td>Y21884 <td>Amino acid sequenc</td> </td>	242	20	Y21884 <td>Amino acid sequenc</td>	Amino acid sequenc
20	848.5	65.8 <td>311</td> <td>9</td> <td>P80151 <td>Multi-functional pr</td> </td>	311	9	P80151 <td>Multi-functional pr</td>	Multi-functional pr
21	843.5	65.4 <td>288</td> <td>20</td> <td>W82743 <td>Fusion protein PNG</td> </td>	288	20	W82743 <td>Fusion protein PNG</td>	Fusion protein PNG
22	843.5	65.4 <td>289</td> <td>20</td> <td>Y06132 <td>Monoclonal antibod</td> </td>	289	20	Y06132 <td>Monoclonal antibod</td>	Monoclonal antibod
23	843.5	65.4 <td>673</td> <td>20</td> <td>W82742 <td>Transferrin CD4/35.15</td> </td>	673	20	W82742 <td>Transferrin CD4/35.15</td>	Transferrin CD4/35.15
24	829	64.3 <td>248</td> <td>19</td> <td>W63830 <td>H and L chain Fv r</td> </td>	248	19	W63830 <td>H and L chain Fv r</td>	H and L chain Fv r
25	828.5	64.3 <td>247</td> <td>14</td> <td>R32091 <td>H and L chain Fv r</td> </td>	247	14	R32091 <td>H and L chain Fv r</td>	H and L chain Fv r
26	828.5	64.3 <td>248</td> <td>20</td> <td>Y17964 <td>Mouse scFv fragmen</td> </td>	248	20	Y17964 <td>Mouse scFv fragmen</td>	Mouse scFv fragmen
27	828.5	64.3 <td>249</td> <td>14</td> <td>R32090 <td>H and L chain Fv r</td> </td>	249	14	R32090 <td>H and L chain Fv r</td>	H and L chain Fv r
28	828.5	64.3 <td>249</td> <td>17</td> <td>R95213 <td>Heavy and light ch</td> </td>	249	17	R95213 <td>Heavy and light ch</td>	Heavy and light ch
29	822.5	63.8 <td>248</td> <td>20</td> <td>Y17960 <td>Mouse scFv fragmen</td> </td>	248	20	Y17960 <td>Mouse scFv fragmen</td>	Mouse scFv fragmen
30	816.5	63.3 <td>305</td> <td>21</td> <td>Y59265 <td>Antibody 4H5 L cha</td> </td>	305	21	Y59265 <td>Antibody 4H5 L cha</td>	Antibody 4H5 L cha
31	816.5	63.3 <td>305</td> <td>21</td> <td>Y51142 <td>Murine derived pro</td> </td>	305	21	Y51142 <td>Murine derived pro</td>	Murine derived pro
32	815.5	63.3 <td>281</td> <td>18</td> <td>W27560 <td>Consensus single c</td> </td>	281	18	W27560 <td>Consensus single c</td>	Consensus single c
33	813	63.1 <td>580</td> <td>20</td> <td>W90217 <td>Bispecific tetra</td> </td>	580	20	W90217 <td>Bispecific tetra</td>	Bispecific tetra
34	812	63.0 <td>365</td> <td>18</td> <td>W35131 <td>R. pipiens recombi</td> </td>	365	18	W35131 <td>R. pipiens recombi</td>	R. pipiens recombi
35	812	63.0 <td>366</td> <td>18</td> <td>W35132 <td>R. pipiens recombi</td> </td>	366	18	W35132 <td>R. pipiens recombi</td>	R. pipiens recombi
36	808.5	62.7 <td>248</td> <td>20</td> <td>Y17965 <td>Mouse scFv fragmen</td> </td>	248	20	Y17965 <td>Mouse scFv fragmen</td>	Mouse scFv fragmen
37	805.5	62.5 <td>253</td> <td>16</td> <td>R72599 <td>Anti-dansyl single</td> </td>	253	16	R72599 <td>Anti-dansyl single</td>	Anti-dansyl single
38	804	62.4 <td>556</td> <td>20</td> <td>W90218 <td>Bispecific tetra</td> </td>	556	20	W90218 <td>Bispecific tetra</td>	Bispecific tetra
39	804	62.4 <td>559</td> <td>19</td> <td>W37132 <td>Anti-Tac(Fv)-PE40</td> </td>	559	19	W37132 <td>Anti-Tac(Fv)-PE40</td>	Anti-Tac(Fv)-PE40
40	804	62.4 <td>599</td> <td>21</td> <td>R87477 <td>Anti-Tac(Fv)-PE40</td> </td>	599	21	R87477 <td>Anti-Tac(Fv)-PE40</td>	Anti-Tac(Fv)-PE40
41	803.5	62.3 <td>249</td> <td>13</td> <td>R21262 <td>pSCFVNL1 encoding</td> </td>	249	13	R21262 <td>pSCFVNL1 encoding</td>	pSCFVNL1 encoding
42	801.5	62.2 <td>263</td> <td>20</td> <td>Y28470 <td>Vh-(Lk)-Vl of anti</td> </td>	263	20	Y28470 <td>Vh-(Lk)-Vl of anti</td>	Vh-(Lk)-Vl of anti
43	799	62.0 <td>599</td> <td>20</td> <td>W95462 <td>Anti-Tac(Fv)-PE40</td> </td>	599	20	W95462 <td>Anti-Tac(Fv)-PE40</td>	Anti-Tac(Fv)-PE40
44	798.5	61.9 <td>260</td> <td>20</td> <td>W95600 <td>Anti-diogxin scFv</td> </td>	260	20	W95600 <td>Anti-diogxin scFv</td>	Anti-diogxin scFv
45	798.5	61.9 <td>260</td> <td>20</td> <td>W89101 <td>Anti-diogxin singl</td> </td>	260	20	W89101 <td>Anti-diogxin singl</td>	Anti-diogxin singl

## ALIGNMENTS

RESULT 1

ID	W60769	standard; Protein; 243 AA.
XX	W60769:	
XX	08-SEP-1998	(first entry)
DE	Single chain antibody (ScFv) 421 that binds to mutant p53 proteins.	
XX	Single chain antibody; ScFv 421; mouse; p53 protein; oligomerisation;	
KW	regulatory domain; p53 mutant; H273; W248; G281;	
KW	p53-dependent trans-activating activity; restoration;	
KW	tumour-suppressing activity; tumour cell; treatment;	
KW	hyper-proliferation; cancer; re-stenosis; ss.	
OS	Mus sp.	
XX		
PN	W09818825-A1.	
PD	07-MAY-1998.	
XX		
PF	27-OCT-1997;	97WO-FR01921.
XX		
PR	29-OCT-1996;	96FR-0013176.
XX		
XX	(RHON) RHONE-POULENC RORER SA.	
PI	Debussche L, Bracco L;	
XX		
XX	WPT. 1998-272140/24.	
DR	N-PSDB; V36236.	
XX		
PT	Restoring p53-dependent trans-activating activity to cell containing	
PT	mutant p53 - by delivering single-chain antibody specific for the	

PT mutant, particularly for treatment of tumours  
 XX  
 PS Claim 5; Page 31; 54pp; French.  
 XX  
 CC The present sequence represents a single chain antibody (scFv) designated  
 CC 421. The antibody binds to an epitope present in the C-terminal region  
 CC of the p53 protein that includes oligomerisation and regulatory domains,  
 CC specifically between positions 320 and 393. scFv 421 is directed against  
 CC p53 mutants, particularly H273, W248 and G281 mutants. When the scFv is  
 CC introduced into cells containing a mutant p53 protein, p53-dependent  
 CC trans-activating activity is restored. scFv 421 is specific for  
 CC p53-mutants that have lost tumour-suppressing activity and are present in  
 CC tumour cells. It is particularly used to treat hyper-proliferation  
 CC associated with these mutants (e.g. cancer and re-stenosis) but may also  
 CC be used in vitro for studying mechanisms of activity of p53 or its mutant  
 CC and to purify or detect p53.  
 XX  
 SQ Sequence 243 AA;  
 Query Match 100.0%; Score 1289; DB 19; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 2e-83;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QVQLQSGAEIVRSASVSLCTASGFNIKDYMHVWKORPEGLMIGWIDPENGDTX 60  
 DB 1 qvqlqsgaeivrsasvslctasgfnlkdymhwkqpegglewlgwidpengdtey 60  
 QY 61 AKRFOGKATMTADTSSNTAYLQSLASDEPTAVYYCNFPGDALDYWGCGTTTVSSGGG 120  
 DB 61 apkfkgkatmtadtsntaylqlslasedptavycnfygdaldywgqgtltvssggg 120  
 QY 121 SGGGSGGGSDVLMQTPLTSLVTIGOPASISCKSSQSLDSDGKTYLMLLQRPQSGP 180  
 DB 121 sgggsgggsgdvlmqtpltlsvtlqgpasiscckssqslsdgktylnmlqrpqsgp 180  
 QY 181 KRLLIVSKLDGVPDRFTGSGSGTDFTLKINRVEAEDLGVIYVCWQGTHSPITFGAGTKL 240  
 DB 181 krllivskldsgvpdrftgsgsgtdftlkinrveaedlgviyvcwgthspitfgagtkl 240  
 QY 241 ETK 243  
 DB 241 etk 243  
 RESULT 2  
 W28491 ID W28491 standard; Protein: 535 AA.  
 AC W28491;  
 XX  
 DT 25-NOV-1997 (first entry)  
 XX  
 DE Human p53 protein variant S-325 encoded by PBC176.  
 XX  
 KW Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;  
 KW substitution; replacement; transactivation; viral protein VP16; HSV;  
 KW anti-oncogene; hyperproliferation; cancer; restenosis; scFv;  
 KW tumour suppression; apoptosis; single chain antibody variable domain.  
 XX  
 OS Chimeric - Homo sapiens.  
 OS Chimeric - Herpes simplex virus.  
 OS Synthetic.  
 OS  
 PN MO9704092-A1.  
 XX  
 PD 06-FEB-1997.  
 XX  
 PF 17-JUL-1996; 96WO-FR01111.  
 XX  
 PR 19-JUL-1995; 95FR-0008729.  
 XX  
 PA (RHON \*) RHONE POULENC RORER SA.

XX Bracco L, Conseiller E;  
 PI  
 XX  
 DR MPI: 1997-132633/12.  
 XX N-PSDB: T86221.  
 XX  
 PT New p53 variants e.g. with oligomerisation domain replaced by  
 PT leucine zipper - useful for treating hyper-proliferative disorders,  
 PT esp. cancer and restenosis  
 XX  
 PS Claim 36; Pages 88-90; 133pp; French.  
 XX  
 CC Claimed variants of protein p53 have at least part of the  
 CC oligomerisation domain deleted and replaced by a leucine zipper  
 CC domain. The mutants preferably also have at least part of the p53  
 CC transactivation domain (amino acids 1-74) deleted and replaced by  
 CC the transactivating domain (TAD) from herpes simplex virus viral  
 CC protein VP16 (amino acids 411-490) or by a protein domain able to  
 CC bind selectively to a transactivator, especially a single-chain  
 CC antibody variable domain (scFv). The present sequence is that of  
 CC a specifically claimed p53 variant designated S-325 and comprising  
 CC a scFv domain, amino acids 75-325 of human wild-type p53 and a  
 CC leucine zipper domain at the C-terminal. The p53 variants are  
 CC more active and more stable tumour suppressors and apoptosis-inducing  
 CC agents than wild-type p53 and are active where the wild-type protein  
 CC is not, i.e. they are not inactivated by dominant negative or oncogenic  
 CC mutants, nor by other cellular proteins (because the leucine zipper  
 CC domain prevents formation of inactive mixed oligomers).  
 XX  
 SQ Sequence 535 AA;  
 Query Match 99.1%; Score 1277; DB 18; Length 535;  
 Best Local Similarity 98.8%; Pred. No. 3.1e-82;  
 Matches 240; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QVQLQSGAEIVRSASVSLCTASGFNIKDYMHVWKORPEGLMIGWIDPENGDTX 60  
 DB 3 qvqlqsgaeivrsasvslctasgfnlkdymhwkqpegglewlgwidpengdtey 62  
 QY 61 AKRFOGKATMTADTSSNTAYLQSLASDEPTAVYYCNFPGDALDYWGCGTTTVSSGGG 120  
 DB 61 apkfkgkatmtadtsntaylqlslasedptavycnfygdaldywgqgtltvssggg 122  
 QY 121 SGGGSGGGSDVLMQTPLTSLVTIGOPASISCKSSQSLDSDGKTYLMLLQRPQSGP 180  
 DB 123 sgggsgggsgdvlmqtpltlsvtlqgpasiscckssqslsdgktylnmlqrpqsgp 182  
 QY 181 KRLLIVSKLDGVPDRFTGSGSGTDFTLKINRVEAEDLGVIYVCWQGTHSPITFGAGTKL 240  
 DB 183 krllivskldsgvpdrftgsgsgtdftlkinrveaedlgviyvcwgthspitfgagtkl 242  
 QY 241 ETK 243  
 DB 241 etk 245  
 RESULT 3  
 W28492 ID W28492 standard; Protein: 535 AA.  
 AC W28492;  
 XX  
 DT 25-NOV-1997 (first entry)  
 XX  
 DE Human p53 protein variant S-325H.  
 XX  
 KW Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;  
 KW substitution; replacement; transactivation; viral protein VP16; HSV;  
 KW anti-oncogene; hyperproliferation; cancer; restenosis; scFv;  
 KW tumour suppression; apoptosis; single chain antibody variable domain.  
 XX  
 OS Chimeric - Homo sapiens.

```

OS Chimeric - Herpes simplex virus.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 361 /note= "Arg residue at position 182 of wild-type
FT p53 has been mutated to His"
XX
XX MO9704092-A1.
XX
XX 06-FEB-1997.
XX
XX 17-JUL-1996; 96WO-FR01111.
XX
XX 19-JUL-1995; 95FR-0008729.
XX
XX (RHON ) RHONE POULENC RORER SA.
XX
XX Bracco L, Conseiller E;
XX
XX WPI; 1997-132633/12.
XX
XX New p53 variants e.g. with oligomerisation domain replaced by
XX leucine zipper - useful for treating hyper-proliferative disorders,
XX esp. cancer and restenosis
XX
XX Claim 36; Page -; 133pp; French.
XX
XX Claimed variants of protein p53 have at least part of the
XX oligomerisation domain deleted and replaced by a leucine zipper
XX domain. The mutants preferably also have at least part of the p53
XX transactivation domain (amino acids 1-74) deleted and replaced by
XX the transactivating domain (TD) from herpes simplex virus viral
XX protein VP16 (amino acids 411-490) or by a protein domain able to
XX bind selectively to a transactivator, especially a single-chain
XX antibody variable domain (scFv). The present sequence is that of
XX a specifically claimed p53 variant designated S-325H and comprising
XX a scFv domain, amino acids 75-325 of human wild-type p53 (but with
XX Arg182 replaced by His) and a leucine zipper domain at the C-terminal.
XX The p53 variants are more active and more stable tumour suppressors
XX and apoptosis-inducing agents than wild-type p53 and are active where
XX the wild-type protein is not, i.e. they are not inactivated by dominant
XX negative or oncogenic mutants, nor by other cellular proteins (because
XX the leucine zipper domain prevents formation of inactive mixed
XX oligomers).
XX (Note: this sequence does not appear in the specification and has
XX been produced by modifying the given sequence of variant V-325).
XX
XX Sequence 535 AA:

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```

Query Match          99.1%; Score 1277; DB 18; Length 535;
Best Local Similarity 98.8%; Pred. No., 3, 1e-82;
Matches 240; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 OVQLOOSGAEIVSGASVSKLTASGFNIDYVMHWKORPEOGLWIGIDPENGSTEX 60
DB 3 qvdlqgeagelavysgasvsklscasgfnldkdyhmhwkqrpqglewlgldpengu 62
QY 61 APRFOGKATMTADTSNTAVYLOLSLASEDTAVYCNFYDADLDYWGQGTTVVSSGGG 120
DB 63 apfkgkatmtadtsntavylqlslasedtavycnfydaldywgqgttvvssggg 122
QY 121 SGGGSGSGGSDVLMOTPTLTISVTIGQPSISGKSSQLDSDGKTYLWMLQRPQSP 180
DB 123 sggsgsgsgsdvlmotptltisvtigqpsisgkssqlsdsgktylmwllqrpqsp 182
QY 181 KRILYVSKSDSGVDPDRFTSGSGTDEFTLKINRVEADLVYVCMQGTSPLEFGAGTKL 240
DB 183 krilyvskidsyvpdrftsgsgtdetlkinrveeadlvyycmggtspplcfigagtkl 242
QY 241 EIK 243
I: I

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DB 243 eik 245
RESULT 4
ID Y06273 standard; Protein: 353 AA.
XX
XX Y06273;
XX
XX 23-AUG-1999 (first entry)
XX
XX Anti Fc alpha receptor scFv A77-PDGR-R TM fusion.
XX
XX Single chain antibody; scFv; A77; IgA receptor; Fc receptor;
XX Fc alpha receptor; platelet derived growth factor receptor;
XX antibody engineering; cell surface expression; therapy; cancer;
XX tumour; vaccine; human.
XX
XX Chimeric - Mus sp.
XX
XX Chimeric - synthetic.
XX
XX Key Location/Qualifiers
XX Domain 1..21 /note= "Ig K-chain SP"
XX Peptide 22..30 /note= "HA epitope"
XX Domain 38..160 /note= "A77 VL"
XX Peptide 161..175 /note= "linker"
XX Domain 176..287 /note= "A77 VH"
XX Peptide 294..303 /note= "Myc epitope"
XX Domain 304..353 /note= "PDGFR transmembrane domain"
XX
XX MO9928349-A2.
XX
XX 10-JUN-1999.
XX
XX 02-DEC-1998; 98WO-US25556.
XX
XX 02-DEC-1997; 97US-0067232.
XX
XX (MEDA-) MEDAREX INC.
XX
XX Deo YM, Goldstein J, Graziano R, Keler T;
XX
XX WPI; 1999-371099/31.
XX
XX N-PSDB; X58936.
XX
XX Cells expressing anti-Fc receptor binding components
XX
XX Example 6; Fig 10A-E; 68pp; English.
XX
XX The present sequence represents a fusion protein comprising murine
XX anti-Fc alpha receptor antibody A77 scFv and the transmembrane domain
XX of platelet derived growth factor receptor (PDGR-R TM). It is
XX encoded by expression vector pUG718 (see X58935). Murine tumour
XX cells transformed to express A77-TM were able to bind a soluble form
XX of the Fc alpha receptor, and the bound receptor was able to engage
XX IgA molecules. This is an example of cells of the invention that
XX have been transformed to express on their surface a component which
XX binds to an Fc receptor of an effector cell. The transformed cell
XX is targeted to an effector cell via the Fc binding component, and
XX can be used as a vehicle to increase an effector cell-mediated
XX immune response, such as cell lysis and phagocytosis, against an
XX antigen associated with the cell. The transformed cells are used
XX to treat cancer and infectious diseases or used as vaccines. The
XX method allows for killing of target cells without targeting any
XX particular antigen on the cell. This is advantageous since many
XX tumour cells and other target cells do not have defined antigens

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五、七

XX This sequence is a used in a method for obtaining a novel gene construct  
CC (A) which expresses, in cells of a mammal, a conjugate (B) of a  
CC cell-tar geting group (I) and a heterologous produg-converting enzyme  
CC (II), and (B) is directed to leave the cell for selective localisation  
CC at a cell surface antigen (Ag) recognised by (I). Delivery of (A) to a  
CC target site, then administration of (III) is used for targeted release o  
CC cytotoxic drug, specifically for treating cancer but also inflammation  
CC such as rheumatoid arthritis. In situ generation of the targeting  
CC antibody increases selectivity, reducing side effects at normal tissue.  
CC The method is applicable to any antibody-directed enzyme produg therapy  
XX system.  
CC  
XX Sequence 281 AA;  
SQ

Query Match	70.7%;	Score 911;	DB 20;	Length 281;
Best Local Similarity	70.4%;	Pred. No. 6.8e-57;		
Matches 1/4; Conservative	27;	Mismatches 36;	Indels 10;	Gaps 3;

QY	1	OVQLQOOSGAELVRSRGASVYKLSCTASGFNRIKQYMHAWKORPEQLEWIGWIDPENGDTX	60
Db	23	evqI,qgsgaelvrsrgasvksktsctsgfnkndymhwkqgpeglwIawIdpengldey	82
QY	61	APKFGKATMTADTSSNTAVYQLQSLASEDTAVYCN--FYGD--ALDYWGQGTVTYVSS	116
Db	83	apKfgrqkAtlaadssmntayIhIsLtsedtaVychvIlyagylamdyvgqtsvavs	142
QY	117	GGGSGGGSGGGSDVLMOTPLTSTWITGGPASICSKSOSLSDSDGKTYINMWLLORP	176
Db	143	ggsgsgggsgsgsgsgqvlvcgspaimaaspkexkltscassv-----Lymwfdqkp	196
QY	177	GQSEKRLLIYVSKLDSGVDPDRFTTSGSGGCTFTLLINRVEADELGVYVYCWQGTSPITFGA	236
Db	197	gtscklIwYstscnIasgyparfsfgsgtsysltIsimeeadaatyccqrstlypltfga	256
QY	237	GTKLEIK 243	
Db	257	gtrleIk 263	

XX	WT	New gene construct expressing conjugate of targeting agent and
XX	DR	N-PSDB; V72075.
XX	MP1:	1999-058700/05.
XX	P1	BlaKey DC, Emery SC;
XX	PA	(ZENEC) ZENECA LTD.
XX	PR	10-MAY-1997; 97GB-0009421.
XX	PF	05-MAY-1998; 98WO-GB01294.
XX	PD	19-NOV-1998.
XX	PN	MO9851787-A2.
XX	OS	Synthetic.
XX	KM	Inflammation; rheumatoid arthritis; antibody; prodrug therapy system
XX	KW	prodrug-converting enzyme; cell surface antigen; treatment; cancer;
XX	KX	Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;
XX	DE	Fusion protein (806.077 scfv-CPGZ)2.
XX	DT	10-MAY-1999 (first entry)
XX	AC	W82745;
XX	ID	W82745 standard; Protein; 666 AA.
XX	RESULT	7

PT	prodrug-converting enzyme - useful for, e.g. targeted production of
PT	cytotoxic drug <i>in vivo</i> , especially for treatment of cancer
XX	
PS	Example 17; Page 87-89; 100pp; English.

CC This sentence is used in a method for obtaining a novel gene construct  
CC (A) which expresses, in cells of a mammal, a conjugate (B) of a  
CC cell-targeting group (I) and a heterologous prodrug-converting enzyme  
CC (II), and (B) is directed to leave the cell for selective localisation  
CC at a cell surface antigen (Ag) recognised by (I). Delivery of (A) to a  
CC target site, then administration of (III) is used for targeted release of  
CC cytotoxic drug, specifically for treating cancer but also inflammation  
CC such as Rheumatoid arthritis. In situ generation of the targeting  
CC antibody increases selectivity, reducing side effects at normal tissue.  
CC The method is applicable to any antibody-directed enzyme prodrug therapy  
CC system.

Query Match	70.7%;	Score 911;	DB 20;	Length 666;
Best Local Similarity	70.4%;	Pred. No. 1.7e-56;		
Matches 174;	Conservative 27;	Mismatches 36;	Indels 10;	Gaps 3

[illegible]

RESULT	8
ID	R75719 Standard; Protein; 270 AA.
XX	
AC	R75719;
XX	
DT	26-JAN-1996 (first entry)
XX	
DE	MFE-23 antibody.
XX	
KW	Antibody; MFE-23; carcinoembryonic antigen; CEA; colorectal tumour therapy; diabody.
XX	
OS	Mus musculus.
XX	
FH	Key
FT	Region
FT	:27..267 "variable region"
FT	/note= "variable heavy chain"
FT	:162..267
FT	; /note= "variable light chain"
FT	:27..51
FT	/note= "FR H1"
FT	:52..61
FT	/note= "CDR H1"
FT	:62..75
FT	/note= "FR H2"

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FT Region 76..85
FT /note= "CDR H2"
FT Region 86..124
FT /note= "FR H3"
FT Region 125..135
FT /note= "CDR H3"
FT Region 136..146
FT /note= "FR H4"
FT Region 147..161
FT /note= "linker"
FT Region 162..184
FT /note= "FR L1"
FT Region 185..194
FT /note= "CDR L1"
FT Region 195..209
FT /note= "FR L2"
FT Region 210..216
FT /note= "CDR L2"
FT Region 217..248
FT /note= "FR L3"
FT Region 249..257
FT /note= "CDR L3"
FT Region 258..267
FT /note= "FR L4"

XX MO9515341-A1.
XX 08-JUN-1995.
XX 05-DEC-1994: 94WO-GB02658.
XX 03-DEC-1993: 93GB-0024807.
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX PA
XX Begent RHJ, Chester KA, Hawkins RE;
XX WPI: 1995-215234/28.
XX DR N-PSDB; Q90663.
XX
XX Antibody for carcinoembryonic antigen - for treatment and diagnosis
XX of colorectal cancer

PS Claim 3; Page 48-49; 72pp; English.
XX
XX This sequence represents the MFE-23 antibody, which is an antibody
XX against carcinoembryonic antigen (CEA). CEA is a marker antigen for
XX cancer imaging and therapy. The MFE-23 antibody sequence was obtained
XX using phage technology. In this process, mice were immunised with CEA.
XX The antibody variable region genes obtained from these mice were then
XX amplified from cDNA and cloned as a single chain Fv (scFv) into
XX bacteriophage vectors, producing a library. The phages that bound to
XX biotinylated CEA were selected and amplified. This sequence (and the
XX encoding cDNA) were selected. This sequence was found to have good
XX specificity and affinity for CEA, meaning that it can be used in targeted
XX anti-tumour therapies. A humanised antibody with the complementarity
XX determining regions of MFE-23 may be produced by CDR grafting. The
XX antibody may be used for the treatment by surgery or therapy of a
XX colorectal tumour, or in the diagnosis of a colorectal tumour. MFE-23
XX may also be used to make diabodies (bivalent or bispecific antibody
XX fragments which bind to two different antigens), and may be linked to an
XX antitumour agent or a detectable label.
XX
XX Sequence 270 AA:

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Query Match 70.3%; Score 906; DB 16; Length 270;
Best Local Similarity 69.2%; Pred. No. 1.5e-56;
Matches 173; Conservative 26; Mismatches 35; Indels 16; Gaps 3;

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```

OY 1 OYOLQSGAEIVSGAVSKISCTASGFNIKIDYVHWVWKORPEGLKIGWIDPENGTLEY 60
DB 27 qvXlqsgaeivsgavskisctasgfnikidsymhwlrqpgqglewlgwldpengdley 86

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OY 61 APRFGKATMETADTSNTAYLQSSIAEDTAVYYCN-----FYGDALDYWGQGTFTV 113
DB 87 aprfgkatfttdtsntaylqssltsedavyycneqgptgpy---fdywgqgtvtc 143
OY 114 VSSGGGGSGGGGGSDVLMQTPTLTLSVTIGQPASISCKSQSLDSDGKTYLNMWL 173
DB 144 vssggsgsgsgsgsdvmlqtpaltmsaspqekvltcasssv-----symhwfq 197
OY 174 QRPQSPKRLIYLVSKDSCVPPDFTSGSGTDTFTLKINRVEAEDLGYYCMQGTHTSPLT 233
DB 198 qkpgtspkrllylvskdscvppdftsgsgtstysltismedaatyycqgrsyplc 257
OY 234 FGAGTKLEIK.243
DB 258 fgagtkleik 267

RESULT 9
W11508
ID W11508 standard; Protein; 553 AA.
XX
XX AC W11508;
XX
XX 24-SEP-1997 (first entry)
XX
XX Single chain anti-Fc gamma RI antibody fused to anti-CEA antibody.
XX
XX Humanised antibody; anti-Fc receptor; H22; bifunctional; bispecific;
XX fusion protein; chimera; carcinoembryonic antigen; CEA.
XX OS Chimeric - Mus musculus.
XX OS Chimeric - Homo sapiens.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..19
XX FT /label= signal_peptide
XX FT Domain 20..139
XX FT /label= H22_VH
XX FT /note= "Anti-Fc gamma RI antibody H22 heavy chain
XX variable domain"
XX FT Region 140..154
XX FT /label= linker
XX FT Domain 155..266
XX FT /label= H22_VL
XX FT /note= "Anti-Fc gamma RI antibody H22 light chain
XX variable domain"
XX FT Region 267..276
XX FT /label= linker
XX FT Domain 277..396
XX FT /label= MFE-23_VH
XX FT /note= "Anti-CEA antibody MFE-23 heavy chain variable
XX domain"
XX FT Region 397..411
XX FT /label= linker
XX FT Domain 412..520
XX FT /label= MFE-23_VL
XX FT /note= "Anti-CEA antibody MFE-23 light chain variable
XX domain"
XX FT Region 521..533
XX FT /label= linker
XX FT Peptide 534..544
XX FT /label= c-myc_tag
XX FT Region 548..553
XX FT /label= His-6_tail
XX FT /note= "6 histidine residues"
XX
XX MO9640789-A1.
XX 19-DEC-1996.
XX PD 96WO-US09988.
XX 07-JUN-1996;

```







RESULT 13  
 ID Y78328 standard; Protein: 532 AA.  
 AC Y78328;  
 DT 04-MAY-2000 (first entry)  
 DE Bispesific anti-zeta-chain/anti-EpCAM antibody protein sequence.  
 XX  
 XX Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;  
 KW complementary determining region; CDR; autoimmune disease; cytostatic;  
 KW immune deficiency; T-cell malignancy; infectious disease; antiviral;  
 KW immunosuppressive; antimicrobial; immune response modulator; NK-cell.  
 XX  
 OS Rattus norvegicus.  
 XX Synthetic.  
 XX WO200003016-A1.  
 XX  
 XX 20-JAN-2000.  
 XX  
 XX 09-JUL-1999; 99WO-EP04838.  
 XX  
 XX 10-JUL-1998; 98EP-0112867.  
 XX  
 XX (CONN-) CONNEX GMBH.  
 XX  
 XX Reiter C;  
 PI  
 PI WPI: 2000-160926/14.  
 DR N-PSDB: 288358.  
 XX  
 XX New oligonucleotide, polypeptide, antibody useful for treating  
 PT autoimmune disease, immune deficiencies, T-cell malignancies and  
 PT infectious diseases -  
 XX  
 XX Example 9; Page 74-76; 79pp; English.

CC The present invention describes a nucleic acid molecule (1) encoding at  
 CC least one complementary determining region (CDR) of a variable region of  
 CC an antibody which specifically interacts with the extracellular domain of  
 CC the human zeta-chain. The antibody whose CDR of a variable region is  
 CC encoded by (1), is obtained by immunising a rat with jurkat cells and  
 CC subsequently with a conjugate comprising a carrier molecule and a  
 CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The  
 CC anti-zeta-chain antibody is useful for the treatment and prevention of  
 CC autoimmune diseases, immune deficiencies, T-cell malignancies,  
 CC infectious diseases and the suppression of immune response preferably in  
 CC order to avoid graft rejection after organ transplantation, malignancies,  
 CC or viral infections. The antibody, and fragments of it, can be useful for  
 CC the enhancement or suppression of NK-cell dependent immunity or for the  
 CC treatment of NK-cell derived malignancies. It can also be useful for the  
 CC determination of zeta-chain or eta-chain expression on NK-cells,  
 CC T-lymphocytes or their precursors. The present sequence represents a  
 CC bispesific anti-zeta-chain/anti-EpCAM antibody, from an example from  
 CC the present invention.  
 XX  
 XX Sequence 532 AA:  
 XX

Query Match 67.4%; Score 869; DB 21; Length 532;  
 Best Local Similarity 47.2%; Pred. No. 1,1e-53;  
 Matches 1/9; Conservative 27; Mismatches 37; Indels 136; Gaps 2;  
 QY 1 QVQLQSGAEIVRSGAVSKLCTASGFNIDYIMHWVKORPEGLWIGWIDPENGSTEX 60  
 DB 142 qvqlqsgaeivrvsgavsklctasgyftfsgymhwikqpgnglewlgwlypgngntky 201  
 QY 61 APFQGGKATMTATSSNTATVLOSSLASEDTANYTC----- 96  
 DB 202 ngkfngkatltadkssstasmjqltsedsavycardwhysyylrpfaywgggtlvt 261

QY 97 ----- 96  
 DB 262 vssggsgsevqlleqsgaelarpgasvklscaksgyftfnyglswvkqrpgvlewlgv 321  
 QY 97 -----NFYGD-----LD 104  
 DB 322 yprlgnaynekfkqkatltadkssstasmelrsltsedsavycarirsgyldnydwfd 381  
 QY 105 YWGCGTTVTVSSGGSGSGGSDVLMQPTLTSLVTIGOPASISCKSSQSLDSD 164  
 DB 382 vwgqgtvtvssggsgsgsgselvmqcplslpvslygdqasiscrsgslvshn 441  
 QY 165 GRTYIMMLQRFQSGSEKRLIVSVSKLDSGVPDRFTGSGSDFTTKINFEADIGVYVC 224  
 DB 442 gntylhwylqkpgspklllykvsnrfsqpdrrfsgsgstfdtlklsrveadlgyvfc 501  
 QY 225 WQGHSPPLTFGAGTKLEIK 243  
 DB 502 sqsthyvylfsgggtkilek 520

RESULT 14  
 ID Y29910 standard; Protein: 348 AA.  
 AC Y29910;  
 XX  
 XX 17-NOV-1999 (first entry)  
 DT  
 DE Human IP-10 and murine scFv20A fusion protein.  
 DE  
 DE Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;  
 KW immune response; HIV; infection.  
 KW  
 XX Homo sapiens.  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 XX WO9946392-A1.  
 XX  
 XX 16-SEP-1999.  
 XX  
 XX 12-MAR-1999; 99WO-US05345.  
 XX  
 XX 12-MAR-1998; 98US-0077745.  
 XX  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 XX Kwak LW, Biragyn A;  
 PI  
 PI WPI: 1999-551418/46.  
 DR  
 XX  
 XX New fusion polypeptides comprising a chemokine and a tumour antigen or  
 PT HIV antigen, used for treating cancers or treating or preventing HIV  
 PT infection -  
 XX  
 XX Disclosure: Page 114-115; 142pp; English.

CC The present invention describes fusion proteins comprising a chemokine  
 CC and a tumour antigen or HIV antigen. Specifically claimed fusion proteins  
 CC comprise: (1) human monocytic chemotactic protein-3 (MCP-3) and human  
 CC Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;  
 CC (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human  
 CC HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV  
 CC gp120. The fusion proteins, and nucleotide sequences encoding them, can  
 CC be used for producing an immune response, e.g. an effector T cell immune  
 CC response. They can also be used for treating cancer or treating or  
 CC preventing HIV infection. The fusion proteins and/or nucleotide sequences  
 CC can be used in in vitro diagnostic assays, as well as in screening assays  
 CC for identifying unknown tumour antigen epitopes and fine mapping of  
 CC tumour antigen epitopes. The present sequence represents a fusion protein  
 CC from the present invention.

```

XX Sequence      348 AA:
SQ
Query Match      67.2%; Score 866; DB 20; Length 348;
Best Local Similarity 65.3%; Pred. No. 1.2e-53;
Matches 160; Conservative 37; Mismatches 46; Indels 2; Gaps 1;

OY 1 OV0LOSGAEIVSSGASVYKLSCTASGFENIKDYMHVVKORPEGLWIMIGIDPENGDTEY 60
   :|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 98 evqlqsgspdlvkgpmsvksckllygnfsdkrlhwkqkpgyglewvgrldpsngdtdy 157

OY 61 APKFGKATMTADTSSNTAVYLOSLASEDTAVYYCNFYGD--ALDYWGQTTVTVSSGG 118
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 158 nadfktpatlvdprpsntaylelsnltsgdsavycisgdsyadcywqggtelvtssgg 217

OY 119 GSGGGGSGGSDVIMTQPLTLSTVIGQPASISCKSSQSLSDSGKTYLNLQRPQ 178
   :|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 218 gsgsgsgsgsgsdvmtqtplslavslgdhvkmscrcnsglvnshgdsflhwflqkpg 277

OY 179 SPKRLIYLVSKLDSGVDREFTGSGGTDFTLKINRVEAEDLGYYCQGTSPFTFGAGT 238
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 278 spklllykvsrffgyperitsgsgsgtdfllelstrveadlgyfcsqgahvpwtlfggt 337

OY 239 KLEIK 243
   :|:|:|
Db 338 klevk 342

RESULT 15
Y29912
ID Y29912 standard; Protein; 361 AA.
XX Y29912:
XX
XX 17-NOV-1999 (first entry)
XX
DE Human MCP-3 and murine scFv20A fusion protein.
XX
XX Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
XX immune response; HIV; infection.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
XX PN MO9946392-A1.
XX
PD 16-SEP-1999.
XX
XX 12-MAR-1999; 99WO-US05345.
XX
XX 12-MAR-1998; 98US-0077745.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kwak LW, Biragyn A;
XX
XX PI
XX
XX DR MPI; 1999-551418/46.
XX
XX PT New fusion polypeptides comprising a chemokine and a tumour antigen, or
XX HIV antigen, used for treating cancers or preventing HIV
XX infection
XX
XX PS Disclosure; Page 116-117; 142pp; English.
XX
XX CC The present invention describes fusion proteins comprising a chemokine
XX and a tumour antigen or HIV antigen. Specifically claimed fusion proteins
XX comprise: (1) human monocytic chemotactic protein-3 (MCP-3) and human
XX Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;
XX (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human
XX SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and
XX HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV

```

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CC gp120. The fusion proteins, and nucleotide sequences encoding them, can
CC be used for producing an immune response, e.g. an effector T cell immune
CC response. They can also be used for treating cancer or treating or
CC preventing HIV infection. The fusion proteins and/or nucleotide sequences
CC can be used in vitro diagnostic assays, as well as in screening assays
CC for identifying unknown tumour antigen epitopes and fine mapping of
CC tumour antigen epitopes. The present sequence represents a fusion protein
CC from the present invention.
XX
SQ Sequence      361 AA:
Query Match      67.2%; Score 866; DB 20; Length 361;
Best Local Similarity 65.3%; Pred. No. 1.2e-53;
Matches 160; Conservative 37; Mismatches 46; Indels 2; Gaps 1;

OY 1 OV0LOSGAEIVSSGASVYKLSCTASGFENIKDYMHVVKORPEGLWIMIGIDPENGDTEY 60
   :|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 111 evqlqsgspdlvkgpmsvksckllygnfsdkrlhwkqkpgyglewvgrldpsngdtdy 170

OY 61 APKFGKATMTADTSSNTAVYLOSLASEDTAVYYCNFYGD--ALDYWGQTTVTVSSGG 118
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 171 nadfktpatlvdprpsntaylelsnltsgdsavycisgdsyadcywqggtelvtssgg 230

OY 119 GSGGGGSGGSDVIMTQPLTLSTVIGQPASISCKSSQSLSDSGKTYLNLQRPQ 178
   :|||||:|:|:~|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 231 gsgsgsgsgsgsdvmtqtplslavslgdhvkmscrcnsglvnshgdsflhwflqkpg 290

OY 179 SPKRLIYLVSKLDSGVDREFTGSGGTDFTLKINRVEAEDLGYYCQGTSPFTFGAGT 238
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 291 spklllykvsrffgyperitsgsgsgtdfllelstrveadlgyfcsqgahvpwtlfggt 350

OY 239 KLEIK 243
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Db 351 klevk 355

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Search completed: February 12, 2001, 15:23:21  
Job time: 36 sec



**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2001, 15:22:50 ; Search time 76.8 seconds

(without alignments)  
477.351 Million cell updates/sec

Title: US-09-297-181-2

Perfect score: 1289

Sequence: 1 QVLOOQSGAEIVRSGASVYL.....CMQGTSPDLFRGAGTKLEIK 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 924906 seqs, 150866555 residues

Total number of hits satisfying chosen parameters: 924906

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Pending\_Patents\_AA:\*

1: /cgn2\_6/ptodata/2/paa/US06.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/paa/US06.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/paa/US07.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/paa/US08.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/paa/US08.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/paa/US08.COMB.pep:\*  
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9: /cgn2\_6/ptodata/2/paa/US08.COMB.pep:\*  
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23: /cgn2\_6/ptodata/2/paa/US09.COMB.pep:\*  
24: /cgn2\_6/ptodata/2/paa/US09.COMB.pep:\*  
25: /cgn2\_6/ptodata/2/paa/US09.COMB.pep:\*  
26: /cgn2\_6/ptodata/2/paa/US09.COMB.pep:\*  
27: /cgn2\_6/ptodata/2/paa/US09.COMB.pep:\*  
28: /cgn2\_6/ptodata/2/paa/US09.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1289	100.0	243	16	US-09-297-181-2
2	1277	99.1	535	13	US-08-983-035-38
3	970.5	75.3	257	18	US-09-419-788-113
4	961	74.6	249	16	US-09-297-181-4
5	930.5	72.2	238	19	US-09-559-019-28

6	926.5	71.9	240	19	US-09-559-019-27	Sequence 27, Appl
7	902	70.0	251	1	PCT-US00-19843-11	Sequence 11, Appl
8	900.5	69.9	271	27	US-09-523-095A-30	Sequence 30, Appl
9	900.5	69.9	274	27	US-09-523-095A-26	Sequence 26, Appl
10	900	69.8	553	17	US-09-364-088-16	Sequence 16, Appl
11	900	69.8	553	19	US-09-523-279-16	Sequence 16, Appl
12	900	69.8	553	27	US-09-188-082-16	Sequence 16, Appl
13	892.5	69.2	245	27	US-09-523-095A-40	Sequence 40, Appl
14	892.5	69.2	271	27	US-09-523-095A-34	Sequence 34, Appl
15	892.5	69.2	274	27	US-09-523-095A-32	Sequence 32, Appl
16	891	69.1	251	1	PCT-US00-19843-15	Sequence 15, Appl
17	891	69.1	264	1	PCT-US00-19843-8	Sequence 8, Appl
18	875.5	67.9	267	18	US-09-419-788-30	Sequence 30, Appl
19	866	67.2	348	20	US-09-646-028-12	Sequence 12, Appl
20	866	67.2	361	20	US-09-646-028-14	Sequence 14, Appl
21	854.5	66.3	242	19	US-09-594-985A-5	Sequence 5, Appl
22	850	65.9	242	16	US-09-202-000-14	Sequence 14, Appl
23	834	64.7	271	19	US-09-594-985A-6	Sequence 6, Appl
24	833.5	64.7	272	19	US-09-594-985A-7	Sequence 7, Appl
25	832	64.5	262	19	US-09-594-985A-4	Sequence 4, Appl
26	829	64.3	248	13	US-08-996-140-23	Sequence 23, Appl
27	828.5	64.3	247	7	US-08-331-396C-34	Sequence 34, Appl
28	828.5	64.3	247	7	US-08-331-396A-34	Sequence 34, Appl
29	828.5	64.3	247	7	US-08-331-397-34	Sequence 34, Appl
30	828.5	64.3	247	7	US-08-331-398-34	Sequence 34, Appl
31	828.5	64.3	247	11	US-08-759-804-34	Sequence 34, Appl
32	828.5	64.3	247	16	US-09-227-693-34	Sequence 34, Appl
33	828.5	64.3	248	7	US-08-331-396C-34	Sequence 34, Appl
34	828.5	64.3	248	7	US-08-331-396D-34	Sequence 34, Appl
35	815.5	63.3	281	14	US-09-025-769B-178	Sequence 178, App
36	813	63.1	580	18	US-09-468-029-58	Sequence 58, Appl
37	809.5	62.8	269	14	US-09-070-408-132	Sequence 132, App
38	809.5	62.8	269	22	US-06-045-409-132	Sequence 132, App
39	805.5	62.5	253	1	PCT-US94-11411-6	Sequence 6, Appl
40	805.5	62.5	253	1	US-08-134-536-6	Sequence 6, Appl
41	805.5	62.5	253	8	US-08-440-764-6	Sequence 6, Appl
42	805.5	62.5	253	12	US-08-838-521-6	Sequence 6, Appl
43	804	62.4	556	18	US-09-468-029-60	Sequence 60, Appl
44	801.5	62.2	263	16	US-09-293-533-66	Sequence 66, Appl
45	799	62.0	239	18	US-09-431-213-8	Sequence 8, Appl

## ALIGNMENTS

RESULT 1  
US-09-297-181-2  
; Sequence 2, Application US/09297181  
; GENERAL INFORMATION:  
; APPLICANT: Bracco, Laurent  
; APPLICANT: Debussche, Laurent  
; TITLE OF INVENTION: ANTI-P53 SINGLE-CHAIN ANTIBODY FRAGMENTS AND THEIR USES  
; FILE REFERENCE: S196030-US  
; CURRENT APPLICATION NUMBER: US/09/297,181  
; CURRENT FILING DATE: 1999-04-26  
; EARLIER APPLICATION NUMBER: PCT/FR97/01921  
; EARLIER FILING DATE: 1997-10-27  
; EARLIER APPLICATION NUMBER: FR96/13176  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentia Ver. 2.0  
; SEQ ID NO 2:  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-297-181-2

Query Match 100.0%; Score 1289; DB 16; Length 243;  
Best Local Similarity 100.0%; Pred. No. 1.3e+102;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QVLOOQSGAEIVRSGASVYLSCFASGFNIKDYMHVWVKRPEGLMIGWIDPENDTEY 60

Db 1 QVOLOSGAELVNSGASVSKLSTASGFNIDYMHVWKORPEQGLEWIGIDPENGDTXY 60  
QY 61 APFGOKATMTADTSSNTATLQSLSLASEDTAVYCNFYGDALDYGQGTTVVSSGGG 120  
Db 61 APFGOKATMTADTSSNTATLQSLSLASEDTAVYCNFYGDALDYGQGTTVVSSGGG 120  
QY 121 SGGGSGGGGSDVLMOTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNMLLQRPQSP 180  
Db 121 SGGGSGGGGSDVLMOTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNMLLQRPQSP 180  
QY 181 KRLLIYVSKLSDGVPDRFTGSGGSDFTLTKINRVEADLGVYCNQGTSPPLTFAGTKL 240  
Db 181 KRLLIYVSKLSDGVPDRFTGSGGSDFTLTKINRVEADLGVYCNQGTSPPLTFAGTKL 240  
QY 241 EIK 243  
Db 241 EIK 243

RESULT 2  
US-08-983-035-38  
Sequence 38, Application US/08983035  
GENERAL INFORMATION:  
APPLICANT: CONSEILLER, Emmanuel  
APPLICANT: BRACCO, Laurent  
TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL  
TITLE OF INVENTION: USES THEREOF  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Road, Wallstop 3043  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/983,035  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/08729  
FILING DATE: 19-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO FR96/01111  
FILING DATE: 17-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Savitzky Esq., Martin F.  
REGISTRATION NUMBER: 29,699  
REFERENCE/DOCKET NUMBER: ST95044-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3816  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ. ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 535 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-983-035-38

Query Match 99.1%; Score 1277; DB 13; Length 535;  
Best local Similarity 98.8%; Pred. No. 3,6e-101;  
Matches 240; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY QVOLOSGAELVNSGASVSKLSTASGFNIDYMHVWKORPEQGLEWIGIDPENGDTXY 60  
|||||

Db 3 QVOLOSGAELVNSGASVSKLSTASGFNIDYMHVWKORPEQGLEWIGIDPENGDTXY 62  
QY 61 APFGOKATMTADTSSNTATLQSLSLASEDTAVYCNFYGDALDYGQGTTVVSSGGG 120  
Db 61 APFGOKATMTADTSSNTATLQSLSLASEDTAVYCNFYGDALDYGQGTTVVSSGGG 122  
QY 121 SGGGSGGGGSDVLMOTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNMLLQRPQSP 180  
Db 121 SGGGSGGGGSDVLMOTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNMLLQRPQSP 182  
QY 181 KRLLIYVSKLSDGVPDRFTGSGGSDFTLTKINRVEADLGVYCNQGTSPPLTFAGTKL 240  
Db 181 KRLLIYVSKLSDGVPDRFTGSGGSDFTLTKINRVEADLGVYCNQGTSPPLTFAGTKL 242  
QY 241 EIK 243  
Db 241 EIK 243

RESULT 3  
US-09-419-788-113  
Sequence 113, Application US/09419788  
GENERAL INFORMATION:  
APPLICANT: FISCHER, Rainer  
APPLICANT: SCHILLBERG, Stefan  
APPLICANT: NAHRING, Jorg  
APPLICANT: SACK, Markus  
APPLICANT: MONECKE, Michael  
APPLICANT: LIANO, Yu-Cal  
APPLICANT: SPIEGEL, Holger  
APPLICANT: ZIMMERMAN, Sabine  
APPLICANT: EMANS, Neil  
TITLE OF INVENTION: Molecular Pathogenetic Mediated Plant Disease  
TITLE OF INVENTION: Resistance  
FILE REFERENCE: 0147-0189P  
CURRENT APPLICATION NUMBER: US/09/419,788  
CURRENT FILING DATE: 1999-10-18  
EARLIER APPLICATION NUMBER: 98 11 9630.6 EP  
EARLIER FILING DATE: 1998-10-16  
EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA  
NUMBER OF SEQ. ID NOS: 163  
SOFTWARE: Patent Ver. 2.1  
SEQ. ID NO 113  
LENGTH: 257  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic, no  
US-09-419-788-113

Query Match 75.3%; Score 970.5; DB 18; Length 257;  
Best local Similarity 77.2%; Pred. No. 2.8e-75;  
Matches 193; Conservative 13; Mismatches 33; Indels 11; Gaps 3;

QY 1 QVOLOSGAELVNSGASVSKLSTASGFNIDYMHVWKORPEQGLEWIGIDPENGDTXY 60  
Db 3 EVOLOSGAELVNSGASVSKLSTASGFNIDYMHVWKORPEQGLEWIGIDPENGDTXY 62  
QY 61 APFGOKATMTADTSSNTATLQSLSLASEDTAVYCNFYGDALDYGQGTTVVSSGGG- 119  
Db 61 APFGOKATMTADTSSNTATLQSLSLASEDTAVYCNFYGDALDYGQGTTVVSSGGG- 118  
QY 120 --GGG--GGGSGGGSDVLMOTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNMLL 173  
Db 120 --GGG--GGGSGGGSDVLMOTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNMLL 178  
QY 174 QRPQSPKRLIYVSKLSDGVPDRFTGSGGSDFTLTKINRVEADLGVYCNQGTSPPL 233  
Db 174 QRPQSPKRLIYVSKLSDGVPDRFTGSGGSDFTLTKINRVEADLGVYCNQGTSPPL 238







```

GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo, et al.
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street, 24th Floor
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,088
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/188,082
FILING DATE: 07-JUNE-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane E.
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: MXI-043CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-7414
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-364-088-16

Query Match          69.8%; Score 900; DB 17; Length 553;
Best Local Similarity 68.7%; Pred. No. 7,7e-69;
Matches 171; Conservative 27; Mismatches 35; Indels 16; Gaps 3;

QY 2 VOLQSGAEIVRSGASYKLSCTASGFNIKDYHMKORPEQGLEWIGWIDPENGDTTEYA 61
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DB 278 IKLQSGAEIVRSGTYSKLSCTASGFNIKDSYHMLRQGPQGLEWIGWIDPENGDTTEYA 337
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 PKFGKATMTADTSSNAYVQLSLASEDTAVYYCN-----FYGDALDYWGQTTVTV 114
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DB 338 PKFGKATFTDTSNAYVQLSLASEDTAVYYCNCGTPTGPTVY---FDYWGQTTVTV 394
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 115 SSGGGSGGGSGGGSDVLTOTPLTSLYTIQSPASISCKSSQSLDSDGKTYLWMLQ 174
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 395 SSGGGSGGGSGGGSENVLTQSPALMSASPGKTYITCSASSV-----SYMHPFOQ 448
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QY 175 RPOGSPRLIYVSKLSDGVDPDRFTSGSGTDTLTKINRYEADLGVYYCMQGTSPLETF 234
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DB 449 KPQTSPLMIYTSNLSAGVPARFSGSGSTSYSLTISRMEADAAATYYCQQRSSYPLTF 508
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QY 235 GAGTKLEIK 243
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 509 GAGTKLEIK 517
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-09-523-279-16
Sequence 16, Application US/09523279
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo et al.
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISES OF ANTI-FC RECEPTOR
```

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TITLE OF INVENTION: BINDING AGENTS
FILE REFERENCE: MXI-043CP3
CURRENT APPLICATION NUMBER: US/09/523,279
CURRENT FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/364,088
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/188,082
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 08/661,052
PRIOR FILING DATE: 1996-07-07
PRIOR APPLICATION NUMBER: 08/484,172
PRIOR FILING DATE: 1995-07-07
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 16
LENGTH: 553
TYPE: PRT
ORGANISM: Mus musculus
US-09-523-279-16

Query Match          69.8%; Score 900; DB 19; Length 553;
Best Local Similarity 68.7%; Pred. No. 7,7e-69;
Matches 171; Conservative 27; Mismatches 35; Indels 16; Gaps 3;

QY 2 VOLQSGAEIVRSGASYKLSCTASGFNIKDYHMKORPEQGLEWIGWIDPENGDTTEYA 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 278 IKLQSGAEIVRSGTYSKLSCTASGFNIKDSYHMLRQGPQGLEWIGWIDPENGDTTEYA 337
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 PKFGKATMTADTSSNAYVQLSLASEDTAVYYCN-----FYGDALDYWGQTTVTV 114
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 338 PKFGKATFTDTSNAYVQLSLASEDTAVYYCNCGTPTGPTVY---FDYWGQTTVTV 394
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 115 SSGGGSGGGSGGGSDVLTOTPLTSLYTIQSPASISCKSSQSLDSDGKTYLWMLQ 174
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 395 SSGGGSGGGSGGGSENVLTQSPALMSASPGKTYITCSASSV-----SYMHPFOQ 448
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 175 RPOGSPRLIYVSKLSDGVDPDRFTSGSGTDTLTKINRYEADLGVYYCMQGTSPLETF 234
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 449 KPQTSPLMIYTSNLSAGVPARFSGSGSTSYSLTISRMEADAAATYYCQQRSSYPLTF 508
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 235 GAGTKLEIK 243
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 509 GAGTKLEIK 517
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-09-188-082-16
Sequence 16, Application US/09188082
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chelarian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1975
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,082
FILING DATE:
PRIOR APPLICATION DATA:
```

```
APPLICATION NUMBER: 08/661,052
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MX1-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-188-082-16
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Query Match 69.8%; Score 900; DB 27; Length 553;
Best Local Similarity 68.7%; Pred. No. 7.7e-69;
Matches 171; Conservative 27; Mismatches 35; Indels 16; Gaps 3;
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QY 2 VOLOQSGAEIVRSGASVKLSCTASGFNKKDYMHVWKORPEQGLEWIGMDPENGDEYA 61
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Db 278 IKLOQSGAEIVRSGTYSKLSCTASGFNKKDYMHVWKORPEQGLEWIGMDPENGDEYA 337
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 PKFGKATMTADTSSNTAVYLQSLASEDTAVYYC-----FYGDALDYGQGTIVTV 114
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 338 PKFGKATMTADTSSNTAVYLQSLASEDTAVYYC-----FYGDALDYGQGTIVTV 394
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 115 SSGGGGGGGGGGGSDVLMOTPLTSLVTIGQPASISCKSSQSLDSDGKTYLWMLQ 174
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 395 SSGGGGGGGGGGGSDVLMOTPLTSLVTIGQPASISCKSSQSLDSDGKTYLWMLQ 448
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 175 RPSGPKRLIYVSKLDSGVDPDRFTSGSGDTFTLKINRYEADLDGVYCCWQTHSPLEF 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 449 RPSGPKRLIYVSKLDSGVDPDRFTSGSGDTFTLKINRYEADLDGVYCCWQTHSPLEF 508
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 235 GAGTKLEIK 243
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 509 GAGTKLEIK 517
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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```
RESULT 13
US-09-523-095A-40
; Sequence 40, Application US/09523095A
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, Naoshi
; APPLICANT: UNO, Shinsuke
; APPLICANT: OH-EDA, Masayoshi
; APPLICANT: KIKUCHI, Yasufumi
; TITLE OF INVENTION: APOPTOSIS-INDUCING SINGLE-CHAIN FV
; FILE REFERENCE: 065678/0102
; CURRENT APPLICATION NUMBER: US/09/523,095A
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: JP 11-63557
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-523-095A-40
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Query Match 69.2%; Score 892.5; DB 27; Length 245;
Best Local Similarity 70.3%; Pred. No. 1.3e-68;
Matches 173; Conservative 29; Mismatches 39; Indels 5; Gaps 2;
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QY 1 OVLOQSGAEIVRSGASVKLSCTASGFNKKDYMHVWKORPEQGLEWIGMDPENGDEY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 OVLOQSGAEIVRSGASVKLSCTASGFNKKDYMHVWKORPEQGLEWIGMDPENGDEY 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
QY 61 APRFGKATMTADTSSNTAVYLQSLASEDTAVYYC---NFYGDALDYGQGTIVTVSSG 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 NEFKFKATLTSDKSSSTTAVMDLSLASEDSAVYYCARGGY--TYDDMGQGTTLTVSSG 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 118 GGGSGGGGGGGSDVLMOTPLTSLVTIGQPASISCKSSQSLDSDGKTYLWMLQRP 177
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 GGGSGGGGGGGSDVLMOTPLTSLVTIGQPASISCKSSQSLDSDGKTYLWMLQRP 179
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 178 QSPKRLIYVSKLDSGVDPDRFTSGSGDTFTLKINRYEADLDGVYCCWQTHSPLEF 237
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 QSPKRLIYVSKLDSGVDPDRFTSGSGDTFTLKINRYEADLDGVYCCWQTHSPLEF 239
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 238 TKLEIK 243
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 240 TKLEIK 245
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```

```
RESULT 14
US-09-523-095A-34
; Sequence 34, Application US/09523095A
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, Naoshi
; APPLICANT: UNO, Shinsuke
; APPLICANT: OH-EDA, Masayoshi
; APPLICANT: KIKUCHI, Yasufumi
; TITLE OF INVENTION: APOPTOSIS-INDUCING SINGLE-CHAIN FV
; FILE REFERENCE: 065678/0102
; CURRENT APPLICATION NUMBER: US/09/523,095A
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: JP 11-63557
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-523-095A-34
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Query Match 69.2%; Score 892.5; DB 27; Length 271;
Best Local Similarity 70.3%; Pred. No. 1.4e-68;
Matches 173; Conservative 29; Mismatches 39; Indels 5; Gaps 2;
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QY 1 OVLOQSGAEIVRSGASVKLSCTASGFNKKDYMHVWKORPEQGLEWIGMDPENGDEY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 OVLOQSGAEIVRSGASVKLSCTASGFNKKDYMHVWKORPEQGLEWIGMDPENGDEY 79
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 APRFGKATMTADTSSNTAVYLQSLASEDTAVYYC---NFYGDALDYGQGTIVTVSSG 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NEFKFKATLTSDKSSSTTAVMDLSLASEDSAVYYCARGGY--TYDDMGQGTTLTVSSG 137
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 118 GGGSGGGGGGGSDVLMOTPLTSLVTIGQPASISCKSSQSLDSDGKTYLWMLQRP 177
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 138 GGGSGGGGGGGSDVLMOTPLTSLVTIGQPASISCKSSQSLDSDGKTYLWMLQRP 197
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 178 QSPKRLIYVSKLDSGVDPDRFTSGSGDTFTLKINRYEADLDGVYCCWQTHSPLEF 237
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 198 QSPKRLIYVSKLDSGVDPDRFTSGSGDTFTLKINRYEADLDGVYCCWQTHSPLEF 257
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
QY 238 TKLEIK 243
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 258 TKLEIK 263
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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```
RESULT 15
US-09-523-095A-32
; Sequence 32, Application US/09523095A
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, Naoshi
; APPLICANT: UNO, Shinsuke
; APPLICANT: OH-EDA, Masayoshi
```

```

1  APPLICANT: KIKUCHI, Yasufumi
2  TITLE OF INVENTION: APOPTOSIS-INDUCING SINGLE-CHAIN FV
3  FILE REFERENCE: 065678/0102
4  CURRENT APPLICATION NUMBER: US/09/523,095A
5  CURRENT FILING DATE: 2000-03-10
6  PRIOR APPLICATION NUMBER: JP 11-63557
7  PRIOR FILING DATE: 1999-03-10
8  NUMBER OF SEQ ID NOS: 40
9  SOFTWARE: PatentIn Ver. 2.1
10 SEQ ID NO 32
11
12 LENGTH: 274
13
14 TYPE: PRT
15
16 ORGANISM: Mus sp.
17
18 US-09-523-095A-32

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Query Match:	69.2%	Score	892.5	DB	27	Length	274
Best Local Similarity:	70.3%	Pred	No. 1.5e-68				
Matches	173	Conservative	29	Mismatches	39	Indels	5
						Gaps	2

QY	1	QVOLOOQSAEELVRSYGASVKLSCTGASGFNIKRYVMHWKORPEOLLEWIGMDPENGETEX	60
Dd	23	OYOLOQOSSELYLKRGASVKMSCKRSGTFAHHVIHMYKQRKGGLBHGITYIPNDSTKY	82
QY	61	APRFQGRATMTADTSNTAYLQLSSLASSEDTRAVYYC--NFYGDALDWMGGITVTIVSSG	117
Dd	83	NEKEFKDRITLTSDKSSFTAYVDMLSSLASSEDNAVYYCARGGY--TYDDMGCGTLTFVSSG	140
QY	118	GGSGGGGGGGGGSDVYMTQTPPLRLSVTIQGPAISCKSSQSLDSDGKIYLMNLORPG	177
Dd	141	GGSGGGGGGGGGSDVYMTQSPLSPVSLGQAASIISCSSQSLSLVHNSNGKITLHMVLDKPG	200
QY	178	QSPKRLLILVSKLDSGVDPDRFTGSGSGTDPLFLKNRYEAEDLGYVCOCWGTHSPLTGAG	237
Dd	201	QSPKLILIKVSNRRSGVDRSRSSGSSTVDPLTLMISRVEAEDLGYYFCFSQHVPYETRGCG	260
QY	238	TKLEIK 243	
Dd	261	TKLEIK 266	

Search completed: February 12, 2001, 15:26:21  
Job time: 211 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2001, 15:22:46 ; Search time 21.01 seconds  
(without alignments)  
207.690 Million cell updates/sec

Title: US-09-297-181-2

Perfect score: 1289  
Sequence: 1 OVQLQSGAEIVRSQASVKL.....CMQGHSPLEFGACTKLEIK 243

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/PCITUS.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/Dackfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	906	70.3	270	US-08-652-507-2	Sequence 2, Appl
2	900	69.8	553	US-08-661-052-16	Sequence 16, Appl
3	843.5	65.4	288	US-09-184-658-63	Sequence 63, Appl
4	828.5	64.3	248	US-08-331-398A-34	Sequence 34, Appl
5	828.5	64.3	248	US-08-331-397B-34	Sequence 34, Appl
6	828.5	64.3	248	US-08-759-804A-34	Sequence 34, Appl
7	812	63.0	365	US-08-875-811-53	Sequence 53, Appl
8	812	63.0	366	US-08-875-811-55	Sequence 55, Appl
9	804	62.4	239	US-08-279-772A-8	Sequence 8, Appl
10	804	62.4	239	US-08-902-486-11	Sequence 11, Appl
11	804	62.4	263	US-08-463-163-3	Sequence 3, Appl
12	801.5	62.2	263	US-08-752-844-66	Sequence 66, Appl
13	798.5	61.9	260	US-08-447-402-1	Sequence 1, Appl
14	795.5	61.7	246	US-08-257-341-7	Sequence 7, Appl
15	795.5	61.7	252	US-08-133-804-4	Sequence 4, Appl
16	795.5	61.7	252	US-08-461-838-4	Sequence 4, Appl
17	795.5	61.7	252	US-08-461-386-4	Sequence 4, Appl
18	795.5	61.7	252	US-08-257-341-5	Sequence 4, Appl
19	776.5	60.2	249	US-08-797-689-18	Sequence 18, Appl
20	770.5	59.8	244	US-08-553-497A-20	Sequence 20, Appl
21	767.5	59.5	242	US-08-553-497A-26	Sequence 26, Appl
22	761	59.0	240	US-08-800-198-8	Sequence 8, Appl
23	761	59.0	240	US-09-296-595-8	Sequence 8, Appl
24	759	58.9	273	US-08-403-853-18	Sequence 18, Appl
25	758.5	58.8	246	US-08-553-497A-24	Sequence 24, Appl
26	757.5	58.6	242	US-08-553-497A-28	Sequence 28, Appl
27	755.5	58.6	244	US-08-553-497A-22	Sequence 22, Appl
28	752.5	58.4	240	US-08-488-113B-148	Sequence 148, Appl

29	752.5	58.4	240	US-08-477-484B-148	Sequence 148, App
30	752.5	58.4	240	US-08-646-360-148	Sequence 148, App
31	752.5	58.4	240	US-08-839-765-148	Sequence 148, App
32	752.5	58.4	240	US-09-136-389-148	Sequence 148, App
33	745	57.8	637	US-08-235-838-16	Sequence 16, Appl
34	744.5	57.8	637	US-08-465-473B-16	Sequence 16, Appl
35	744.5	57.8	282	US-08-860-174A-10	Sequence 10, Appl
36	740	57.4	241	US-08-235-838-11	Sequence 11, Appl
37	740	57.4	241	US-08-465-473B-11	Sequence 11, Appl
38	736.5	57.1	277	US-08-256-780-2	Sequence 2, Appl
39	731.5	56.7	483	US-08-392-338A-19	Sequence 19, Appl
40	731.5	56.7	483	US-09-166-750-19	Sequence 19, Appl
41	731.5	56.7	483	US-09-166-093-19	Sequence 19, Appl
42	731.5	56.7	483	US-09-172-019-19	Sequence 19, Appl
43	731.5	56.7	483	US-09-166-094-19	Sequence 19, Appl
44	727	56.4	252	US-08-894-922A-14	Sequence 14, Appl
45	727	56.4	271	US-08-894-922A-10	Sequence 10, Appl

## ALIGNMENTS

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RESULT 1
US-08-652-507-2
; Sequence 2, Application US/08652507
; Patent No. 5876691
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Nixon & Vanderhye, P.C.
; STREET: 1100 No. 5876691th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,507
; FILING DATE: 02-Jul-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Arthur R. Crawford
; REGISTRATION NUMBER: 25,327
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4100
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-507-2

Query Match 70.3% Score 906; DB 2; Length 270;
Best Local Similarity 69.2% Pred. No. 6.8e-66;
Matches 173; Conservative 26; Mismatches 35; Indels 16; Gaps 3;

QY 1 OVQLQSGAEIVRSQASVKLSTAGSPFNKDYVMVQORPGLGEMIGWDPEGDTREY 60
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Db 27 OVQLQSGAEIVRSQASVKLSTAGSPFNKDYVMVQORPGLGEMIGWDPEGDTREY 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 APFGKATMTADTSNTAYLQSLASDPAVYCN-----FYGDALDYWGCGTIVT 113
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Db 87 APRKQKATFTTDTSSNTAYLQSLTSEDTAVAYCNEGTPTGPY--FDYWGQGTYYT 143  
QY 114 VSSGGGGGGGGGGGGGGGSDYLMOTPTLLSVTIGOPASICKSSQSLDSDGKTYLNLWLL 173  
Db 144 VSSGGGGGGGGGGGGGGGSENVLTQSPALMSASGKTYITCSASSV-----SYNHWQ 197  
QY 174 QRPQSPKRLIYVSKLSDGVPPDFTGSGSGDTFTLKINVEAEDLGVIYCWGTHSPLT 233  
Db 198 QKPGTSPKLMYISTSNLASCVPARFSGSGGSGTSTSLTISHMEADATYYCCQRRSSYPLT 257  
QY 234 FGAGTKLEIK 243  
Db 258 FGAGTKLEIK 267

RESULT 2  
US-08-661-052-16  
Sequence 16, Application US/08661052  
Patent No. 5837243

GENERAL INFORMATION:  
APPLICANT: Yashwant M. Deo  
APPLICANT: Joel Goldstein  
APPLICANT: Robert Graziano  
APPLICANT: Chezia Somsundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
City: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/661,052  
FILING DATE:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/484,172  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 533 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-661-052-16

Query Match 69.8%; Score 900; DB 2; Length 553;  
Best Local Similarity 68.7%; Pred. No. 4,8e-65;  
Matches 171; Conservative 27; Mismatches 35; Indels 16; Gaps 3;

QY 2 VOLQSGALVNSGASVKTSCASGNINIKDYHAWVKORPQGLEWIGWIDPENGDTYEA 61  
Db 278 IRLQSGALVNSGASVKTSCASGNINIKDYHAWVKORPQGLEWIGWIDPENGDTYEA 337  
QY 52 PRFQGAATMTADSSNTAYLQSLTSEDTAVAYCNEGTPTGPY--FDYWGQGTYYT 114  
Db 338 PRFQGAATMTADSSNTAYLQSLTSEDTAVAYCNEGTPTGPY--FDYWGQGTYYT 394

QY 115 SSGGGGGGGGGGGGGGGSDYLMOTPTLLSVTIGOPASICKSSQSLDSDGKTYLNLWLLQ 174  
Db 395 SSGGGGGGGGGGGGGGGSENVLTQSPALMSASGKTYITCSASSV-----SYNHWQ 448  
QY 175 RQPGSPKRLIYVSKLSDGVPPDFTGSGSGDTFTLKINVEAEDLGVIYCWGTHSPLT 234  
Db 449 KPGTSPKLMYISTSNLASCVPARFSGSGGSGTSTSLTISHMEADATYYCCQRRSSYPLT 508  
QY 235 GAGTKLEIK 243  
Db 509 GAGTKLEIK 517

RESULT 3  
US-09-184-658-63  
Sequence 63, Application US/09184658  
Patent No. 6030792

GENERAL INFORMATION:  
APPLICANT: Oetters, Ivan G.  
APPLICANT: Mezes, Peter S.  
APPLICANT: Downs, James T.  
APPLICANT: Johnson, Kimberly S.  
TITLE OF INVENTION: Assays for Measurement of Protein Fragments in  
FILE REFERENCE: PC9946-A  
CURRENT FILING DATE: 1998-11-02  
EARLIER APPLICATION NUMBER: 60/065,423  
NUMBER OF SEQ ID NOS: 69  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 63  
LENGTH: 289  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: 5109 VH - VL  
OTHER INFORMATION: scfv.  
FEATURE:  
LOCATION: (1)..(22)  
OTHER INFORMATION: pcANTAB6 signal peptide; Val at position 1 is most  
FEATURE:  
LOCATION: (23)..(138)  
OTHER INFORMATION: 5109 VH domain.  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (139)..(154)  
OTHER INFORMATION: 16 amino acid linker.  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (155)..(266)  
OTHER INFORMATION: 5109 VL domain.  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (270)..(279)  
OTHER INFORMATION: myc tag.  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (284)..(289)  
OTHER INFORMATION: His tag.  
US-09-184-658-63

Query Match 65.4%; Score 843.5; DB 3; Length 289;  
Best Local Similarity 68.4%; Pred. No. 7.9e-61;  
Matches 167; Conservative 23; Mismatches 53; Indels 1; Gaps 1;

QY 1 QVOLQSGALVNSGASVKTSCASGNINIKDYHAWVKORPQGLEWIGWIDPENGDTYEA 60  
Db 23 EVQLVESGGGSGVQPGSKLSCASGFTFTYGMVWVROTDPKRLAEWATINSNGLATFY 82

RESULT 4  
US-08-331-398A-34  
; Sequence 34, Application US/08331398A  
; Patent No. 5608039

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1      TITLE OF INVENTION:  Single Chain B3 Antibody Fusion Proteins
2      TITLE OF INVENTION:  and Their Uses (as amended)
3      NUMBER OF SEQUENCES:  68
4      CORRESPONDENCE ADDRESS:
5      ADDRESSEE:  Townsend and Townsend and Crew
6      STREET:  One Market Plaza, Stewart Street Plaza
7      CITY:  San Francisco
8      STATE:  California
9      COUNTRY:  USA
10     ZIP:  94105-1492
11     COMPUTER READABLE FORM:
12     MEDIUM TYPE:  Floppy disk
13     COMPUTER:  IBM PC compatible
14     OPERATING SYSTEM:  PC-DOS/MS-DOS
15     SOFTWARE:  PatentIn Release #1.0, Version #1.30
16     CURRENT APPLICATION DATA:
17     APPLICATION NUMBER:  US/08/331,398A
18     FILING DATE:  28-OCT-1994
19     CLASSIFICATION:  435
20     PRIOR APPLICATION DATA:
21     APPLICATION NUMBER:  US 07/767,331
22     FILING DATE:  30-SEP-1991
23     PRIOR APPLICATION DATA:
24     APPLICATION NUMBER:  US 07/596,289
25     FILING DATE:  12-OCT-1990
26     ATTORNEY/AGENT INFORMATION:
27     NAME:  Hunter, Tom
28     REGISTRATION NUMBER:  38,498
29     REFERENCE/DOCKET NUMBER:  015280-126110US
30     TELECOMMUNICATION INFORMATION:
31     TELEPHONE:  (415) 543-9600
32     TELEFAX:  (415) 543-5043
33     INFORMATION FOR SEQ ID NO:  34:
34     SEQUENCE CHARACTERISTICS:
35     LENGTH:  248 amino acids
36     TYPE:  amino acid
37     TOPOLOGY:  linear
38     MOLECULE TYPE:  protein
39     US-08-331-398A-34

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Query Match	64.38;	Score 828.5;	DB 1;	Length 248;
Best Local Similarity	63.78;	Pred. No. 1.1e-59;		
Matches 156;	Conservative 34;	Mismatches 52;	Indels 3;	Gaps 1

RESULT 5  
US-08-331-397B-34  
; Sequence 34, Application US/08331397B

APPLICANT: Pastan, Ira  
APPLICANT: Benhar, Itai  
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-  
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses  
TITLE OF INVENTION: thereof  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Street Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,397B  
FILING DATE: 128-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA: US 07/596,289  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOC# NUMBER: 015280-126120US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEO ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 248 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-331-397B-34

Query Match	64.3%	Score 828.5;	DB 2;	Length 248;
Best Local Similarity	63.7%	Pred. No. 1.1e-59;		
Matches 156;	Conservative 34;	Mismatches 52;	Indels 3;	Gaps 1











[illegible]

RESULT 14  
 US-08-257-341-7  
 Sequence 7, Application US/08257341  
 Patent No. 5525491  
 GENERAL INFORMATION:  
 APPLICANT: HUSTON, JAMES S  
 APPLICANT: OPPERMAN, HERMANN  
 APPLICANT: TIMSHEFF, SERGE N  
 TITLE OF INVENTION: SERINE RICH PEPTIDE LINKER  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CREATIVE BIOMOLECULES, INC./PATENT DEPT.  
 STREET: 35 SOUTH STREET  
 CITY: HOPKINTON  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 01748  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/257,341  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/842,149  
 FILING DATE:  
 APPLICATION NUMBER: US 07/662,226  
 FILING DATE: 27-FEB-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CAMPBELL, ESO, PAUL A  
 REGISTRATION NUMBER: 32,503  
 REFERENCE/DOCKET NUMBER: CRP-064CP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/248-7000 (ATTY)  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 246 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-257-341-7

[illegible]

RESULT 15  
 US-08-133-804-4  
 Sequence 4, Application US/08133804  
 Patent No. 5534254  
 GENERAL INFORMATION:  
 APPLICANT: Huston, James S.  
 APPLICANT: Oppermann, Hermann  
 APPLICANT: Houston, L. L.  
 APPLICANT: Ring, David B.  
 TITLE OF INVENTION: Biosynthetic Binding Proteins For  
 TITL OF INVENTION: Imaging  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department  
 STREET: Exchange Place, 53 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/133,804  
 FILING DATE:  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kelley, Robin D.  
 REGISTRATION NUMBER: 34,637  
 REFERENCE/DOCKET NUMBER: 2054/22  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-248-7477  
 TELEFAX: 617-248-7100  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 252 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-133-804-4



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2001, 02:00:11 ; Search time 936.51 Seconds  
(without alignments)  
5589.469 Million cell updates/sec

Title: US-09-297-181-3

Perfect score: 747  
Sequence: 1 caggtcaagctgcagagatc.....gcaccaagctggaatcaaa 747

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	221.4	29.6	641	90	AM4056821
3	214	28.6	533	95	AM802126
4	207	27.7	508	90	AM406572
5	206	27.6	630	90	AM406512
6	205.4	27.4	643	89	AM390292
7	204.4	27.3	358	136	BE850886
8	203.8	27.3	550	90	AM404610
9	202.2	27.1	644	106	BE281961
10	201.6	27.0	388	97	AM951579
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12	200.4	26.8	328	90	AM406484
13	199	26.6	464	107	BE368025
14	196.8	26.3	406	139	BF016722
15	193.6	25.9	459	89	AM383565
16	192.4	25.8	911	106	BE286958
17	190.4	25.5	379	96	AM908776
18	190.4	25.5	542	90	AM405977
19	190	25.4	349	97	AM947280
20	188.4	25.2	512	139	BF023434
21	186.2	24.9	460	90	AM406939
22	185.2	24.8	397	38	AV685287
23	185.2	24.8	401	38	AV685285
24	184.6	24.7	625	38	AV702633
25	184.2	24.7	739	106	BE284158
26	183.4	24.6	449	90	AM402364
27	182.6	24.4	443	139	BF015986
28	180.8	24.2	554	174	A2505978
29	180.6	24.2	363	5	AA300651
30	180.6	24.2	473	106	BE307170
31	179	24.0	323	90	AM407858
32	177.4	23.7	567	106	BE287568
33	177.4	23.7	596	106	BE310080
34	176.8	23.7	364	145	T27579
35	175.8	23.5	601	172	A2447391
36	175	23.4	549	139	BF022578
37	173.2	23.2	439	104	BE136816
38	172.2	23.1	594	106	BE309592
39	172	23.0	517	90	AM408270
40	171.8	22.9	488	90	AM403591
41	171.4	22.9	435	90	AM402541
42	169	22.6	448	90	AM402665
43	168.4	22.5	477	90	AM403686
44	166.4	22.3	398	87	AM429526
45	165.4	22.1	457	90	AM405627

## ALIGNMENTS

RESULT 1  
 BE306420  
 LOCUS BE306420 1057 bp mRNA  
 DEFINITION 601103347F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:3495755 5',  
 mRNA sequence.  
 ACCESSION BE306420  
 VERSION BE306420.1 GI:9159604  
 KEYWORDS EST.  
 SOURCE house mouse.





FEATURES	source
REFERENCE	1. 508
AUTHORS	/organism="Homo sapiens"
TITLE	/db_xref="taxon:9606"
JOURNAL	/clone_image="3060307"
COMMENT	/clone_id="NH_MGC_37"
	/tissue_type="lymph"
	/cell_type="germinal center B cells"
	/cell_line="MGC85"
	/lab_host="DH10B (LTI)"
	/note="Vector: pRT3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT	115 a 139 c 126 g 128 t
ORIGIN	
Query Match	27.7%; Score 207; DB 90; Length 508;
Best Local Similarity	76.4%; Pred. No. 1,7e-50;
Matches 268; Conservative	0; Mismatches 80; Indels 3; Gaps 1;
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49	ggtgctcaccgagggacatgcatgataccacagctcagactcctgagctgctgctgagcc 108
460	gagaaagtcgtatgagctgcaaatccacagtcgaagctcgttcaacagatgaaccggaag 519
109	gagagggccacacatcaatcgaagtcacagccacagagctgtttatcagagctccacaatga 168
520	aatactatgctgtgtatcagcagaacacagggagctcctctaagtcgtatcactgag 579
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RESULT 5
LOCUS   AM406512      630 bp      mRNA      EST      16-FEB-2000
DEFINITION   UI-HF-BL0-acu-a-09-0-UI-r1 NIH_MGC_37 Homo sapiens CDNA clone
IMAGE:3060017 5', mRNA sequence.
ACCESSION   AM406512
VERSION     AM406512.1  GI:6925569
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 630)
AUTHORS     NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            CDNA Library Preparation: M.B. Soares Lab
            CDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/BLNL at:
            www.bio.lnl.gov/db/ftp/image/image.html
            Seq primer: M13 forward.
FEATURES
Source     location/Qualifiers
            1..630
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:3060017"
            /clone_1ib="NIH_MGC_37"
            /tissue_type="lymph"
            /cell_type="germinal center B cells"
            /cell_line="WGC85"
            /lab_host="DH10B (LT1)"
            /note="Vector: pT7T3-Pac; Site.1: NotI; Site.2: Eco RI;
            Constructed from size fractionated cytoplasmic mRNA
            (1.5-2.5kb). Directionally cloned. Cells provided by Louis
            M. Staudt, Ph.D. Library preparation by Maria de Fatima
            Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      162 a      178 c      156 g      134 t
ORIGIN
Query Match      27.6%; Score 206; DB 90; Length 630;
Best Local Similarity 75.4%; Pred. No. 3.5e-50;
Matches 270; Conservative 0; Mismatches 85; Indels 3; Gaps 1;
      393 ctctggcggtggcgagatcgacatgagctcacacagcttcctcttcctgctgctgctc 452
      1 CACGAGGGGTCCTACCGGGACATCGATGACCCAGCTCTCCAGACTCCCTGCTGTGTC 60
      453 agcagaagagaaggtcgctatgagctgcaaatccagtcagagctgctgcaacagtagaac 512
      61 TCTGGGGGAGAGGGCCACATCACTGCAAGTCCAGCCAGACAGCTTTTATACAGCTCCA 120
      513 cgaagaagaatctactgctggtatcagcagaacaacagggcagctctcctaagtgctgat 572

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      121 CAATAAGAAATTTCTAGTTTGGTACGACGAGAAACGACAGACCTCTTAAGCTGCTCAT 180
      573 ctactgggcatccacatcagggaatcgtgagctccctgactgcttcaacagagtgatcctg 632
      181 TTCTTGGGCAATCAACCCGGGAATCCGGGTCTCTGACCCGATTGAGTGCGACGGCTCG 240
      633 gacagattctactctcacatcagcagtgctgcaagctggaagacttgcagtttacttactg 692
      241 GACAGATTTCACTCTCACTCAACATGACAGCCTGCAGGCTGGAAGATGTGGCAGTTTATAC 300
      693 caagcaatctataactctac---gacgttcgcyggyggccacgaagcttgaaatcaaa 747
      301 TCAGCAATATTAATGATATTCCTTCACTTCCTGGCCACAGGACACGATGAGATTAAA 358

RESULT 6
LOCUS   AM390292      643 bp      mRNA      EST      04-FEB-2000
DEFINITION   CM2-ST0182-221099-023-f04 ST0182 Homo sapiens CDNA, mRNA sequence.
ACCESSION   AM390292
VERSION     AM390292.1  GI:6894951
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 643)
AUTHORS     HCGP http://www.ludwig.org.br/ORESTES.
TITLE       The FAPESP/LICR Human Cancer Genome Project
JOURNAL     Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM2&t2=CM2-ST0182-
            221099-023-f04&t3=1999-10-22&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 7
            High quality sequence stop: 641.
FEATURES
Source     location/Qualifiers
            1..643
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_1ib="ST0182"
            /dev_stage="Adult"
            /note="Organ: stomach; Vector: puc18; Site.1: SmaI;
            Site.2: SmaI; A mini-library was made by cloning products
            derived from ORESTES PCR (U.S. Letters Patent application
            No. 196,716 - Ludwig Institute for Cancer Research)
            profiles into the puc 18 vector. Reverse transcription of
            tissue mRNA and cDNA amplification were performed under
            low stringency conditions."
BASE COUNT      162 a      173 c      162 g      146 t
ORIGIN
Query Match      27.5%; Score 205.4; DB 89; Length 643;
Best Local Similarity 76.1%; Pred. No. 5.3e-50;
Matches 267; Conservative 0; Mismatches 81; Indels 3; Gaps 1;
      400 gttgcygagatcggaattgagctcacccagcttcctcttcctgctgctgctgcaagga 459
      57 GGTGCTTAGG36GACATCGTATGACCCAGCTCTCCAGATCCCTGCTGTGCTCTGCGC 116
      460 gagaaggtcgctatgagctgcaaatccagtcagagctgcttcaacagtagaacccgaag 519
      117 GAGAGGGCCACCATCAACTGCAAGTCCAGCAGAGTATTTATACAACTCAAAATAAG 176

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QY	520	aattcttgcttgctgatacagaacacacagggcagcttccctaaagtgcgtactc	579
Db	177	AACTACTTAGCTTGGTACACAGCAGAAACACAGACGACCTCTTAAGTGTCTTTTACTGG	236
QY	580	gatacactcaggaatctgtagtccctgtatcgtcttcacagcagtagtgcattggtggacagat	639
Db	237	GCATCTACCGGAAATCCGGGGCTCCCTGACCCGATTCAGTTCAGTGCAGCGGCTCGACAGAT	296
QY	640	ttcactcttaccatcagcagctgtgcagcgttgaaagacctggcagttattactctcaagcaa	659
Db	297	ATCAGCTCTACCATCAGCAGCCCTGCAGGCTGGAAGATGTGGCACTTTATTACTCTCAGAG	356
QY	700	ttctata---atctaccagcgttcggcggggagccacagctgaatctcaaa	747
Db	357	TATTTTAGTCATCTCAAAAGCTTCGGCCCAAGGACCAAGGTGGAATCAAA	407
RESULT	7		
BE850886	358 bp	MRNA	EST
LOCUS	uw98h05.y1	Soares_mammary_gland	NMLMG Mus musculus cDNA clone
DEFINITION	IMAGE:3469209.5	' similar to SW:HV07_MOUSE P01751	IG HEAVY CHAIN V
ACCESSION	REGION B1-8/186-2	PRECURSOR.	RNA sequence.
VERSION	BE850886		
KEYWORDS	BE850886.1	GI:10309225	
SOURCE	EST.		
ORGANISM	house mouse.		
REFERENCE	Mus musculus		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
JOURNAL	1 (bases 1 to 358)		
COMMENT	NCI-CCAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .		
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP).		
	Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Tel: (301) 496-1550		
	Email: Robert.Strausberg@nih.gov		
	This clone is available royalty-free through LNL ; contact the		
	IMAGE Consortium ( <a href="mailto:info@image.lnl.gov">info@image.lnl.gov</a> ) for further information.		
	MG11388569		
FEATURES	Seq primer: -40RP from Gibco.		
source	Location/Qualifiers		
	1..358		
	/organism="Mus musculus"		
	/db_xref="taxon:10090"		
	/clone="IMAGE:3469209"		
	/clone_lib="Soares_mammary_gland_NMLMG"		
	/sex="female (lactating)"		
	/tissue_type="mammary gland"		
	/lab_host="DH10B"		
	/note="Vector: pRT73D-Pac (pharmacia) with a modified		
	polylinker. 1st strand cDNA was prepared from mammary		
	gland tissue from a lactating female, and was then primed		
	with a Not I - Oligo(dT) primer. Double-stranded cDNA was		
	ligated to Eco RI adaptors (Pharmacia), digested with Not		
	I and cloned into the Not I and Eco RI sites of the		
	modified pRT73 vector. Library is normalized. Library		
	was constructed by Bento Soares and M. Fatima Bonaldo."		
BASE COUNT	89 a 97 c 93 g 79 t		
ORIGIN			
Query Match	27.4%	Score 204.4; DB 136; Length 358;	
Best Local Similarity	74.7%	Pred. No. 8.8e-50;	
Matches	272; Conservative	0; Mismatches 86; Indels 6; Gaps 1	
QY	1	cagttcaagctgcaggaagtcagggcagaactctgtgaggttcagggcctcagtcatttg	60
Db	1	CAGGTCCCAACTCCACAGCAGCCTGGGCTGAGCTGTGAACCTGGGGCTTCAGTCAAGCTG	60
QY	61	tcctgcagagcttcgtgctcaaatataagactactatagtcaactgggtgaaacagag	120

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Db      61 TCTGTCAAGGCGTTTCGGGTACACGCTTCCACGACTGTGATGCAATGGGTAAACAGAGG 120
        |||||
Oy      121 cctgaagagggccttgtagtggatgtgatatattgatctcctgagaatggtgaaactgataat 180
        |||||
Db      121 CCTGGAACAGGCCTTGATGATGCAATCGAAGAAGATTGATCCTTGATAGCTAATACTAAC 180
        |||||
Oy      181 gccccgaacttcacagggcaagagcccctgtgactgtgaagacacatcctccaacagaccac 240
        |||||
Db      181 AATCAAAGTTCMAAGGCAAGGCCACATGTAAGTAGACACATCTCCAAGCACACCCTCAC 240
        |||||
Oy      241 ctgaaccacgaagacctacatcatgaagacaacacgccttaactgaatgcaagtcac 300
        |||||
Db      241 ATGCAAGCTCACAGGCTGACATCATGAGACAATCTGGGGTCTATTACTGT-----GCAACC 294
        |||||
Oy      301 tactatgaatcgcagcgctatgctttggaactactgtgggccaaaggaccaggtcacgc 360
        |||||
Db      295 TAGGTAATFACCTACGAGAGACTACTTGTACTGACTGGGCCCAAGGCACACATCTCACAGT 354
        |||||
Oy      361 tcct 364
        |||||
Db      355 TCCT 358
        |||||

RESULT      8
AM404610    550 bp      mRNA          EST          16-FEB-2000
LOCUS       AM404610
DEFINITION UT-HF-BL0-acc-a-06-0-UT.r1 NIH_MGC_37 Homo sapiens CDNA clone
IMAGE:3058451 5' , mRNA sequence.
ACCESSION   AM404610
VERSION     AM404610.1 GI:6923667
KEYWORDS    EST.
SOURCE      Human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 550)
AUTHORS    NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel.: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            CNSA Library Preparation: M.B. Soares Lab
            CDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNLN at:
            www-bio.lnlnl.gov/dbp/image/image.html
            Seq primer: M13 Forward.

FEATURES             Location/Qualifiers
     source           1..550
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /clone_id="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTR)"
     note             /note=Vector: pT73-Pac; Site.1: NotI; Site.2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldi, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT      140 a      150 c      139 g      121 t
ORIGIN
Query Match      27.3%: Score 203.8; DB 90; Length 550;
Best Local Similarity 75.8%; Pred. NO. 1.5e-49;

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Matches	266: Conservative	0: Mismatches	82: Indels	3: Gaps		
Qy	400	gtgtgcgagatcgtgacattagctacccaagcttcacattccctgtgtgtcgaaga	459			
Db	10	GGTGGCTTACGGGGACATCTGTGATGACCCAGTCTCCAGACTCCTGGCTGTCTGGGC	69			
Qy	460	gagaagatcgtcatgtgcgcgaatccagtcagagctgttcaacagtagaacccgaag	519			
Db	70	GAGAGGGCCACCATCAACACGCAAGTCCACCGACAGAGTGTTTATACAGCTCCACATTAAG	129			
Qy	520	aattccttggttgatcatcagaagaaccagggcagttccttaagtgctgatactatg	579			
Db	130	AACTACTTGTAGCTTGGTATCCAGCAGAAACCAAGACACACTCTCTAACTGCTCATTTATCGGG	189			
Qy	580	gcatccacacagggaatcttgtagtcccttgctgcttaacaggcagtgtagctggaaagt	639			
Db	190	GGATCATCCCGGGAAATCCGGGGCTCCTGTACCCGATTACGTGACGTGGCAGTGGACAT	249			
Qy	640	ttcactctcaccatcagcagctgtgcagcgttgaagacctgtgcagtttatacttcaagca	699			
Db	250	TTTACATCTCACCATCAGCAGCGCTGACGGCTGAAGATGTGGCACTTTATTTATGTCCAA	309			
Qy	700	tcttataatctacc---gaagttcggcgaggggacccaagctggaatcaaa	747			
Db	310	TATTATAGTACTCCATCATCCTTGGCCCAAGGGACACAGCTGGAGATTAA	360			
RESULT 9						
LOCUS	BE281961	644 bp	mRNA	EST 13-JUL-2000		
DEFINITION	601099518p1 NCI_CGAP_Lu29	Mus musculus	CDNA clone	IMAGE:3492028 5'		
ACCESSION	BE281961	mRNA sequence.				
VERSION	BE281961.1	GI:9157200				
KEYWORDS	EST.					
SOURCE	house mouse.					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
TITLE	1 (bases 1 to 644)					
JOURNAL	NIH-MGC <a href="http://www.ncbi.nlm.nih.gov/MGC/">http://www.ncbi.nlm.nih.gov/MGC/</a> .					
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)					
	Unpublished (1999)					
	Contact: Robert Strausberg, Ph.D.					
	Tel: (301) 496-1550					
	Email: Robert.Strausberg@nih.gov					
	Tissue Procurement: Gilbert Smith, Ph.D.					
	CDNA Library Preparation: Life Technologies, Inc.					
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)					
	DNA Sequencing by: Incyte Genomics, Inc.					
	Clone distribution: MGC clone distribution information can be					
	found through the I.M.A.G.E. Consortium/LLNL at:					
	<a href="http://image.llnl.gov">http://image.llnl.gov</a>					
	Plate: LRAM8537 row: c column: 05					
	High quality sequence stop: 561.					
FEATURES	Location/Qualifiers					
SOURCE	1..644					
	/organism="Mus musculus"					
	/strain="C57BL/6J II (fetal)"					
	/db_xref="taxon:10090"					
	/clone="IMAGE:3492028"					
	/clone_lib="NCI_CGAP_Lu29"					
	/tissue_type="spontaneous tumor, metastatic to mammary.					
	Stem cell origin"					
	/lab_host="DH10B"					
	/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;					
	Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.					
	library constructed by Life Technologies. Investigator					
	providing samples: Gilbert Smith, NIH"					
BASE COUNT	147 a 176 c 155 g 166 t					
ORIGIN						

Query Match	27.1%	Score 202.2	DB 106	Length 644
Best Local Similarity	73.5%	Pred. NO. 4.7e-49		
Matches 274	Conservative 0	Mismatches 93	Indels 6	Gaps 1
QY 1	caggtcaagctgtcagagagtcaggggcagaactgtgtaggtcaggggccctcagtcacatttg 60			
Db 63	CAGGTTCCAGCTGCACCAAGCTGCACCTGAGTTGGTGACACCTGGAGCTTCAGTAAGATA 122			
QY 61	tcctgtcaaacgcttcctgggttcaacattaaagactctatctgcatggtgtgtaaacagag 120			
Db 123	TCCTGCACAGGTTCTGGGTGCTACCTTCCTGACCCACTACTACTACTGCTGGGTGAAGCAGAG 182			
QY 121	ccgtgaagaggccctgtagtgatgtgataattgtacctgagagtggtgtaaacatgaatat 180			
Db 183	CCTGAAACAGGGGCGCTGAGATGATGATGATATATTATTTCCTGAGAGATGATGATCTAAGTAC 242			
QY 181	gcccgaacattccaggcgaaggccacatctgtactgcagacacatctctccaaacagcctac 240			
Db 243	AATGAGAAGTTCTCAAGGGCAGAGGCCCACTTGAATGCAGATAAATTCCTCCAGCACTGCTTC 302			
QY 241	ctgcacccctcagcagcctgtacatctgtgagacacaaacgcgtctattactgt-----aatga 294			
Db 303	ATGCAGCTCAACAGCCTACATCTAAGATTTCTGCAGTATTTTCTGTGCCAAGAGGGGGA 362			
QY 295	gtcacactactaagaaacagagcgtatgctttgtgactactgtgggccaagagaccagcgtc 354			
Db 353	TCCATCTACTATAGGTTAGCGCCTCTACTACTTTGACTACTGGGGCCAAAGGCCACCACTATC 422			
QY 355	aaccgtctccag 367			
Db 423	ACAGTCTCTCAG 435			

RESULT	10
AM951579	
LOCUS	AM951579; 388 bp mRNA EST 01-JUN-2000
DEFINITION	EST363649 MAGE resenceses, MAGB Homo sapiens cDNA, mRNA sequence.
ACCESSION	AM951579
VERSION	AM951579..1 GI:8141256
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 388)
AUTHORS	Hedde, P., Qi, R., Abernathy, K., Daarap, S., Gasparid, R., Gay, C., Holt I.E., Sneed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J. Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray unpublished (2000) Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: jhnq@tigr.org Plate: 29
TITLE	
JOURNAL	
COMMENT	Seq primer: Reverse. Location/Qualifiers . . . 1. 388 ./organism="Homo sapiens" ./db_xref="taxon:9606" ./clone_lib="MAGE resenceses, MAGB" ./note="Vector: pBluescriptKm"
BASE COUNT	87 a 110 c 97 g 94 t
ORIGIN	
Query Match	27.0%; Score 201.8; DB 97; Length 388;
Best Local Similarity	75.6%; Pred. No. 5.3e+49;
Matches 264; Conservative	0; Mismatches 82; Indels 3; Gaps 1

QY	400	ggagcgagatcgagacatgaaatcaacacagctcatcatctccctggctgtgtctcaagga	455
Db	40	GGTGCTTAGGGGGAGACCGCTATGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGC	99
QY	460	gagaagtgctgatatgagctgcaaatccagtcagagctctgttcaacaagtacgaaccgaag	515
Db	100	GAGAGGGCCACATCAATATGCAAGTCCAGCCAGAGTGTTTAGACAGCTCCACAATATACG	155
QY	520	aattactgtgcttgttalcagcagaacacgaaggagctctcttaagtgtgctatctatg	575
Db	160	AACCTACTAGCTGTGGTACCAACTGAACAGACAGACGCTCTTAAGCTGTGCTATTACTGG	215
QY	580	gcattccactaaggaaatctgtagagctccctgatactgtctcaagcagatgatactggacgat	635
Db	220	GCATCTACCCGGGAAATCCGGGGGTCCCTGACCGATTTCAGTGTGACACGGGGTCTGGGACAGAT	275
QY	640	ttcactctcacacatcagcagagtgtgcaggtctaaagaaacctggaattttactgaaacaa	695
Db	280	TTCACTCTCAACCTCCAGCGGCTCGAGGCTGAAGAATGGGAGTTTATTACTGTCAACAA	335
QY	700	tcttataatctacgg---agcttggcgcggggaccaaagctggaataca	745
Db	340	TATTATTACTCCGTACAATTTTGGCCAGGGGACCAAGCTGGGAAATCA	388

RESULT 11	
LOCUS	BF015548
DEFINITION	BF015548 507 bp mRNA EST 10-OCT-2000 IMAGE:3658670 5
	uv23aa08.y1 NC1_CGAP_Lu30 Mus musculus cDNA clone IMAGE:3658670 5

ACCESSION	BF015548	
VERSION	BF015548.1	GI:10746880
KEYWORDS	EST.	

**SOURCE ORGANISM**

REFERENCE  
AUTHORS  
TITLE  
1 (Pages 1 to 507)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

**JOURNAL** Unpublished (1997)  
**COMMENT** Contact: Robert Strausberg, Ph.D.

Email: [Robert.Strausberg@nih.gov](mailto:Robert.Strausberg@nih.gov)  
Tissue Procurement: Gilbert Smith, ph.D.  
cDNA library Preparation: Life Technologies, Inc.  
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:  
[image.llnl.gov/image/html/resources.shtml](http://image.llnl.gov/image/html/resources.shtml)

MGI:1421142  
Seq primer: -40RP from GIBCO  
High quality sequence stop: 456.

FEATURES

SOURCE

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L.:30/
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="3658670"
/clone_lib="NCI-CGAP_Mu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="Dh10B"

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BASE COUNT  
ORIGIN

Query Match	27.0%;	Score 201.6;	DB 139;	Length 507;
Best Local Similarity	73.6%;	Pred. No. 6.6e-49;		
Matches 271; Conservative	0;	Mismatches 94;	Indels 3;	Gaps 1;

[illegible]

RESULT	12
AM406484	
LOCUS	AM406484 - 328 bp mRNA EST 16-FEB-2000
DEFINITION	UT-HR-BD0-scr-f-09-0-U-T1 NIH.MGC_37 Homo sapiens cDNA clone IMAGE:3060232 5', mRNA sequence.
ACCESSION	AM406484
EERSION	AM406484.1 GI:6925541

ORGANISM	REFERENCE
Homo sapiens	Chordata: Craniata: Vertebrata: Euteleostomi: Eukaryota; Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia; Eutheria: Primates: Catarrhini: Hominae: Homo. 1 (bases 1 to 328)
NH-MGC	<a href="http://www.ncbi.nlm.nih.gov/MGC/">http://www.ncbi.nlm.nih.gov/MGC/</a>
National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.	

Email: Robert.Strausberg@nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: M.B. Soares Lab  
cDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www.dio.llnl.gov/dbfp/image/image.html](http://www.dio.llnl.gov/dbfp/image/image.html)  
Seq primer: M13 Forward.

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FEATURES
source
location/Qualifiers
1. .328
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3060232"
/clone_1lb="NH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="McG85"
/lab_host="DH10B (LTI)"
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/note="Vector: pT73-Pac; Site\_1: NotI; Site\_2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(1.5-2.5kb). Directionally cloned. Cells provided by Louis  
M. Staude, Ph.D. Library preparation by Maria de Fatima  
Bonafide, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 78 a 92 c 84 g 74 t

Query Match 26.8%; Score 200.4; DB 90; Length 328;  
Best Local Similarity 79.5%; Pred. No. 1.3e-48;  
Matches 237; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 411 ggcattgagctaccaccagctccatctccctgctgctgctgagcagagagctcgc 470  
DB 15 ggacatcgtatataccacagctccacagctccctgctgctgctgagcagagc 74  
QY 471 tatgagctgcaatccagctcagctgctgctcagctgagacccgaaagattactg 530  
DB 75 catcaactgcagatccagcagagctgctgctgctcagctcagcagcagctgagc 134  
QY 531 ttggtatcagcagaaacagcagctcctcctaaagctgctgctgctgagcagc 590  
DB 135 ttggtatcagcagaaacagcagctcctcctaaagctgctgctgagcagcagc 194  
QY 591 ggcattgagctaccaccagctccatctccctgctgctgctgagcagagctcgc 650  
DB 195 ggacatcgtatataccacagctccacagctccctgctgctgctgagcagagc 254  
QY 651 catcagcagctgctgagcagctgagcagctgagcagctgagcagcagcagc 708  
DB 255 catcagcagctgctgagcagctgagcagctgagcagctgagcagcagcagc 312

RESULT 13  
BE368025 464 bp mRNA EST 21-JUL-2000  
LOCUS 601221914F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:3590907 5',  
DEFINITION mRNA sequence.  
ACCESSION BE368025  
VERSION BE368025.1 GI:9313388  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
TITLE NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L14M8759 row: k column: 04  
High quality sequence stop: 462.

FEATURES  
source location/Qualifiers  
1.464

/organism="Mus musculus"  
/strain="C57BL/6J (f1)"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3590907"  
/tissue\_type="spontaneous tumor, metastatic to mammary."  
/stem\_cell\_origin="Stem cell origin."  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site\_1: SalI;

Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"

BASE COUNT 119 a 118 c 109 g 118 t

Query Match 26.6%; Score 199; DB 107; Length 464;  
Best Local Similarity 72.9%; Pred. No. 3.8e-48;  
Matches 272; Conservative 0; Mismatches 95; Indels 6; Gaps 1;

QY 1 caggtcaagctcgaagcagcagcagcagcagcagcagcagcagcagcagcagc 60  
DB 72 caggtcaagctcgaagcagcagcagcagcagcagcagcagcagcagcagcagc 131  
QY 61 tectgacagctctgctgctcagcagcagcagcagcagcagcagcagcagcagc 120  
DB 132 tctgacagctctgctgctcagcagcagcagcagcagcagcagcagcagcagc 191  
QY 121 cctgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180  
DB 192 cctgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 251  
QY 181 ggcattgagctaccaccagctccatctccctgctgctgctgagcagagctcgc 240  
DB 252 ggacatcgtatataccacagctccacagctccctgctgctgctgagcagagc 311  
QY 241 cgtgacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 294  
DB 312 atgcacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 371  
QY 295 gtcattctatgataacagcagcagcagcagcagcagcagcagcagcagcagc 354  
DB 372 tccattctatgataacagcagcagcagcagcagcagcagcagcagcagcagc 431  
QY 355 accgtctcctcag 367  
DB 432 acagctcctcctcag 444

RESULT 14  
BF016722 406 bp mRNA EST 10-OCT-2000  
LOCUS uy34h12.y1 NCI\_CGAP\_Lu30 Mus musculus cDNA clone IMAGE:3660143 5',  
DEFINITION similar to SM-HV02\_MOUSE P01746 IG HEAVY CHAIN V REGION 9367  
PRECUSOR. ; mRNA sequence.  
ACCESSION BF016722  
VERSION BF016722.1 GI:10748054  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
TITLE NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/  
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
COMMENT Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
image.llnl.gov/image/html/resources.shtml

FEATURES  
source location/Qualifiers  
1.406  
Seq primer: -40RP from Gibco.  
Location/Qualifiers  
1.406

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/organism="Mus musculus"
/strain="C2ECH II"
/db.xref="taxon:10090"
/clone.lib="IMAGE:3660143"
/clone.lib="NCI_CGAP_Lu30"
/tissue.type="tumor; metastatic to mammary"
/lab.host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: SalI; transgenic model MMTV-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

```

BASE COUNT 109 a 102 c 97 t

```

/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone.lib="HT0348"
/dev.stage="Adult"
/notes="Organ: head,neck; Vector: puc18; Site:1: SmaI;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

BASE COUNT 110 a 123 c 118 g 107 t 1 others

Query Match 26.3%; Score 196.8; DB 139; Length 406;  
 Best Local Similarity 80.2%; Pred. No. 1.6e-47;  
 Matches 231; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Query Match 25.9%; Score 193.6; DB 89; Length 459;  
 Best Local Similarity 78.5%; Pred. No. 1.5e-46;  
 Matches 245; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

QY 1 caggtcaagctcagagagcagagagctgtgagctcagagagcctcagctatgtg 60  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 93 CAGGTCACGCTGCAGCAGTCTGGGGCTGAGTGCACAAACCTGGGGCTCAGTAAGATG 152  
 QY 61 tccctcagagctctcgtctcaacattaaagactactatgacactggtgaaacagag 120  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 153 TCCTGCAAGGCTTCTGCTGACCTTACTAGTACTGATGACACTGGTAAACAGAGG 212  
 QY 121 cctgaagagagcctcgtggtggtatgtatattcctcgaagagtggtgaactgaaat 180  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 213 CCTGGACAGGCTCTGAGATGATGATACATTAATCCTAGCACTGGTATACTGAGTAC 272  
 QY 181 gccccgaactcagagcagagcagcagctgacgtcagacacacatcctcaacagagctac 240  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 273 AATCAGAGATTCAAGAGCAAGAGCCACATTGACTGACACAAATCTCTCAGCAGACGCTAC 332  
 QY 241 ctgcacctcagcagcctgacatctgaggacacacacgcgtctattactgt 288  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 333 ATGCAACTGAGACCTGACATCTGAGAGACTGCTCAGTCTATTTACTGT 380

## RESULT 15

AM383565 459 bp mRNA EST 04-FEB-2000  
 LOCUS PM4-HT0348-261199-001-B1 HT0348 Homo sapiens cDNA, mRNA sequence.  
 DEFINITION  
 ACCESSION AM383565  
 VERSION AM383565.1 GI:6888133  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 459)  
 HGGP <http://www.ludwig.org.br/ORESTES>.  
 The FAPESP/LICR Human Cancer Genome Project.  
 Unpublished (1999)  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?fl=PM4&lt2=PM4-HT0348-261199-001-B1&lt3=199-11-26&lt4=1>)  
 Seq primer: puc 18 forward  
 High quality sequence start: 10  
 High quality sequence stop: 441.  
 Location/Qualifiers  
 1. 459

Search completed: February 18, 2001, 02:00:14  
 Job time: 13898 sec

QY 439 tccctgctgtgtcagcagagagagagtcgtatgagctcaaatccagctcagagctgtg 498  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 16 TCCTGGCTGTGCTCTGCTGGCGAGTGGCCACCATCACTGCAAGTCCAGCCAGGGTCTT 75  
 QY 499 tcaacagtagaacccgaagaattacttgctgtgtatcagcagaacacagagcagctc 558  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 76 TTGTACAGCTCCACCAATAGAACTACTTGGCTGTACACGACGAGAACCCAGCAGCCT 135  
 QY 559 cctaaagtgctgtactcgtggtgacacacaggaagcagctcgtgagctcctcagctcaca 618  
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 Db 136 CTAAGGCTGCTCAATTACTGCGCATCTACCCGGGAATCCGGGCTCCCTGACCATTCAGT 195  
 QY 619 ggcagtgatctgtgagcagattcactcctcaccatcagcagctgtgcaagctgaagacgtg 678  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 196 GGCAGGGGGCTGGGACAGATTCTCACTCACCATCAGACAGAGCCTGAGGCTGAAGATGTG 255  
 QY 679 gcaatttactgacgaacatcttaatactacg---acgttcggcgggggacccaag 735  
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 Db 256 GCAGTTTATTTACTGTCACAAATATTATTTAGTACTCGCTCACTTTCGCGAGGACCAAG 315  
 QY 736 ctggaatcaca 747  
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 Db 316 GTGGAGATCANA 327

FEATURES  
 source .  
 1. 459  
 Location/Qualifiers



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2001, 15:24:31 ; Search time 42.85 seconds  
(without alignments)  
681.092 Million cell updates/sec

Title: US-09-297-181-4  
Perfect score: 1315  
Sequence: 1 QVKLQESGALVRSAGAVNL.....YKQSYNLPFGGKTLEIK 249

Scoring table: BROSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP-REMBL\_15:\*  
2: sp-archaea:\*  
3: sp-bacteria:\*  
4: sp-fungi:\*  
5: sp-human:\*  
6: sp-invertebrate:\*  
7: sp-mammal:\*  
8: sp-mhc:\*  
9: sp-phage:\*  
10: sp-plant:\*  
11: sp-rodent:\*  
12: sp-virus:\*  
13: sp-vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	744.5	56.6	298	11 Q9YF0	Q9YF0 mus musculus
2	433.5	33.0	109	11 Q9JL85	Q9JL85 mus musculus
3	384	29.2	118	11 Q9Z1C4	Q9Z1C4 mus musculus
4	379.5	28.3	117	11 Q9QX69	Q9QX69 mus musculus
5	374	28.4	107	4 Q9JL81	Q9JL81 homo sapien
6	370	28.4	124	4 Q9JL92	Q9JL92 homo sapien
7	370	28.1	109	4 Q9JL78	Q9JL78 homo sapien
8	368.5	28.0	99	11 Q9JL74	Q9JL74 mus musculus
9	368.5	28.0	108	4 Q9JL70	Q9JL70 homo sapien
10	368	28.0	110	11 Q9JL77	Q9JL77 mus musculus
11	367.5	27.9	117	11 Q9QX60	Q9QX60 mus musculus
12	367	27.9	114	11 Q9JL81	Q9JL81 mus musculus
13	365.5	27.8	108	4 Q9JL79	Q9JL79 homo sapien
14	363.5	27.6	108	4 Q9JL77	Q9JL77 homo sapien
15	359	27.3	109	11 Q9JL75	Q9JL75 mus musculus
16	355	27.0	109	4 Q9JL85	Q9JL85 homo sapien
17	351.5	26.7	108	4 Q9JL83	Q9JL83 homo sapien
18	349.5	26.6	119	4 Q9JL94	Q9JL94 homo sapien
19	348.5	26.5	125	4 Q9JL95	Q9JL95 homo sapien

20	347.5	26.4	150	4 Q9Y298	Q9Y298 homo sapien
21	342	26.0	104	11 Q9JL82	Q9JL82 mus musculus
22	338	25.7	109	4 Q9JL86	Q9JL86 homo sapien
23	334.5	25.4	117	11 Q9Z1C6	Q9Z1C6 mus musculus
24	334.5	25.4	214	11 Q9JL85	Q9JL85 mus musculus
25	331.5	25.2	114	4 Q9JL80	Q9JL80 homo sapien
26	313.5	23.8	101	11 Q9JL78	Q9JL78 mus musculus
27	311.5	23.7	103	11 Q9JL80	Q9JL80 mus musculus
28	309.5	23.5	107	11 Q9JL84	Q9JL84 mus musculus
29	309	23.5	116	4 Q9JL89	Q9JL89 homo sapien
30	306	23.3	110	11 Q9JL83	Q9JL83 mus musculus
31	306	23.3	147	4 Q9Y509	Q9Y509 homo sapien
32	305.5	23.2	113	4 Q9JL90	Q9JL90 homo sapien
33	305	23.2	106	5 Q9JL10	Q9JL10 schistosoma
34	302.5	23.0	131	4 Q9JL88	Q9JL88 homo sapien
35	301.5	22.9	116	4 Q9JL93	Q9JL93 homo sapien
36	300.5	22.9	119	4 Q9JL73	Q9JL73 homo sapien
37	300.5	22.9	121	4 Q9JL71	Q9JL71 homo sapien
38	296.5	22.5	97	11 Q9JL76	Q9JL76 mus musculus
39	296.5	22.5	157	4 Q9JL97	Q9JL97 homo sapien
40	288.5	21.9	109	6 Q9JL05	Q9JL05 oryctolagus
41	286	21.7	150	4 Q9JL91	Q9JL91 homo sapien
42	285	21.7	118	4 Q9JL91	Q9JL91 homo sapien
43	285	21.7	118	4 Q9JL72	Q9JL72 homo sapien
44	284	21.6	124	6 Q9JL06	Q9JL06 oryctolagus
45	282	21.4	124	6 Q9JL04	Q9JL04 oryctolagus

## ALIGNMENTS

RESULT 1  
Q9YF0 PRELIMINARY: PRT: 298 AA.  
AC Q9YF0  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE CN 8 SCFV.  
GN CN 8.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BALB/C; TISSUE-SPLEEN;  
RA Shiohara N., Demura T., Fukuda H.;  
RT Isolation of a novel type of vascular cell wall-specific monoclonal  
RT antibody recognizing a cell polarity using a phase display subtraction  
RT method.";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB036341; BAA8633.1; -;  
DR HSSP: P01607; IRL.  
DR INTERPRO: IPR003006; -;  
DR PFM: PFM0047; Ig: 2.  
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 56.6%; Score 744.5; DB 11; Length 298;  
Best Local Similarity 56.4%; Pred. No. 7.4e-58;  
Matches 141; Conservative 37; Mismatches 61; Indels 11; Gaps 3;

QY 1 QVKLQESGALVRSAGAVNLCTASGFNKKDYMHVKKRPEGLWIGTIPSESETTY 60  
DB 40 QVKLQESGALVRSAGAVNLCTASGFNKKDYMHVKKRPEGLWIGTIPSESETTY 99  
QY 61 APNFGKATVFTDSSNTAYVHLISLTSBTDYVYCNNAVYVEYDGYALDYWGQGTTVTV 120

[illegible]

RESULT	2
ID	09JL85
AC	09JL85
DT	01-OCT-2000 (TReMBLrel_15, Created)
DT	01-OCT-2000 (TReMBLrel_15, Last sequence update)
DT	01-OCT-2000 (TReMBLrel_15, Last annotation update)
DE	ANTI-MYOSIN IMMUNOLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
OX	NCHI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BALB/C;
RA	Malkiel S., Liao T., Cunningham M.W., Diamond B.;
RT	"Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RL	acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
DR	Submitted (NOV-1999) to the EMBL/GenBank/DDBF databases.
EMBL:	AF206021; AF69319.1; -.
FT	NON_TER
FT	NON_TER
Q	SEQUENCE
	109 AA: 109
	109 AA: 11944 MW: DFE615FEC6CDAEDE CRC64:

Query Match	33.0%	Score 433.5	DB 11	Length 109
Best Local Similarity	70.9%	Pred. 4.9e-31		
Matches 83	Conservative 11	Mismatches 12	Indels 11	Gaps
QY	9	AEVYSGASVNLSTCTAGSGFNKDYMHVWQREEGLEWIGYIDPESGETEYAPNFQKA	68	
Db	1	AEVKKPGASVYKLSCTAGSGFNEDYMHVWQREEGLEWIGYIDPAPFGSHKDYKPKQGA	60	
QY	69	TVVADTSSNTAYVHLHSLTSEDTTVYC--NAVITYEDGVALDYWGQGTIVVSS	122	
Db	61	TVVSDTSSNTAYVQLSLTSEDTAYVYCVRRGAVV-----DYWGQGTALTVSS	109	
RESULT	3			
Q9Z1C4		PRELIMINARY;	PRT;	118 AA.
ID	Q9Z1C4			
AC	Q9Z1C4;			
DT	01-MAY-1999 (TrEMBLrel. 10, Created)			
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last annotation update)			
DE	ANTI-PORCINE VCAAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eultheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.			
OX	NCBI_TaxID-10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	STRAIN-BALB/C;			
RC	McKeller J.P., Gianoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,			
RT	Matis L.M., Evans M.J.;			
RT	"Humanized porcine VCAAM-specific monoclonal antibodies with chimeric			
RT	1962/64-constant regions block human leukocyte binding to porcine			

RT endothelial cells";  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases  
 DR EMBL: U78801; ADD00293.1; -.  
 DR INTERPRO: IPR003006; -.  
 DR PFAM: PF00047; Pf: 1.  
 FT NON\_TER 1  
 FT NON\_TER 118  
 FT NON\_TER 118  
 SQ SEQUENCE 118 AA, 13036 MW, 90DEEC559D31EC4FC CRC64;

Query Match	29.2%	Score 384;	DB 11;	Length 118;
Best Local Similarity	62.3%	Pred. No. 1.2e-26;		
Matches 76; Conservative	13;	Mismatches 29;	Indels 4;	Gaps 2

[illegible]

RESULT	4	
090X69		
ID	090X69	PRELIMINARY; PRT; 117 AA.
AC	090X69;	
DT	01-MAY-2000 (TRIMBLrel. 13, Created)	
DT	01-MAY-2000 (TRIMBLrel. 13, Last sequence update)	
DT	01-JUN-2000 (TRIMBLrel. 14, Last annotation update)	
DE	IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	
CC	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Clemens A., Rademakers A., Specht C., Koelisch E.;	
RL	Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AJ225174; CAB5237.1; -	
DR	INTERPRO; IPR003006; -	
DR	PFAM; PF000047; Ig; 1. 1.	
FT	NON_TER	1
FT	NON_TER	117
FT	NON_TER	117
QQ	SEQUENCE	117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

	Query Match:	28.9%	Score	379.5;	DB	11;	Length	117;
	Best Local Similarity	59.8%;	Pred. No.	3e-26;				
	Matches	73;	Conservative	17;	Mismatches	27;	Indels	5; Gaps
								1
QY	1 QVXLOESGAEIVKSGASVNLSCITASGFNIKDYMHMWKQREPEGLEWIGYIDBEGSETEY	60						
DQ	1 EVQLDQSGEVLVKPGASVYMCKASKAGYIFETDYMKWAKWSHGKSLIEWIGIDINPNNGTSY	60						
QY	61 AAFPGOKATVTADTSSNNTVAIHLSSLTSEDPTTYVCNAVIYYIEDGDALDYWGQTIVY	120						
DB	61 NQFKKKRALTVDKRSSSTAIYMQLNLSLTEDSAVYYCANDRY----	115						
QY	121 SS 122							
DB	116 SS 117							
RESULT	5							
ID	Q9ULR1							
AC	Q9ULR1;							
DT	01-MAY-2000 (TREMBLrel. 13, Created)							
	PRELIMINARY;							
	PRT;							
	107 AA.							

DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus".  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035033; AAD56269.1; -.  
 DR HSSP; P0362; 1MTL.  
 DR MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
 DR PFAM; PF00047; 19; 1.  
 FT NON\_TER 1 1  
 FT SEQUENCE 107 107 11501 MW; 070549FDE0754748 CRC64;  
 SQ

Query Match 28.4%; Score 374; DB 4; Length 107;  
 Best Local Similarity 61.6%; Pred. No. 8.2e-26;  
 Matches 69; Conservative 22; Mismatches 15; Indels 6; Gaps 1;

OY 138 DIELTOSPSLAVSAGEKVMKSSOSLFSNRKRYLAWYQKQKQSPKLYIWASTR 197  
 DB 1 DIQMTQSPSLASVSGDRVITICRASQSI-----SNYLWYQKQKQKAPNLLIYASSL 54  
 OY 198 EGVGPRFTGSGSGDTFTLTISVQAEDLAVYCKOSYNLPTFGGKLEIK 249  
 DB 55 QSGVPRFSGSGSGDTFTLTISGLQAEDEFTYCCQSYSLPTFGKVIDR 106

RESULT 6  
 O9UL92 PRELIMINARY; PRT; 124 AA.  
 AC 09UL92;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
 DT 01-JUN-2000 (TREMBLrel. 14, last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus".  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035022; AAD56238.1; -.  
 DR INTERPRO; IPR003006; -.  
 DR PFAM; PF00047; 19; 1.  
 FT NON\_TER 1 1  
 FT SEQUENCE 124 124 13580 MW; 1BAACBD96ACD2A2 CRC64;  
 SQ

Query Match 28.4%; Score 373; DB 4; Length 124;  
 Best Local Similarity 56.5%; Pred. No. 1.2e-25;  
 Matches 70; Conservative 16; Mismatches 36; Indels 2; Gaps 1;  
 OY 1 QVTLSSGALVSGSYNSCTASGFNIDYIMHWKQPEEGLEWIGITDEPSETET 60  
 DB 1 EYLVESGAEVKKPGASVSKASGYTFSSYYIMHWVROAPGGGLEMGIIINSGSTSY 60

OY 61 ADFQKATVADTSSNTAYLHLSLTSSEDTVYVCNAVYYEYD--YALDYGQGTIV 118  
 DB 61 ADFQKATVADTSSNTAYLHLSLTSSEDTVYVCNAVYYEYD--YALDYGQGTIV 120  
 OY 119 TVSS 122  
 DB 121 TVSS 124

RESULT 7  
 O9UL78 PRELIMINARY; PRT; 109 AA.  
 AC 09UL78;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus".  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035036; AAD56272.1; -.  
 DR HSSP; P01789; 1MCP.  
 DR INTERPRO; IPR003006; -.  
 DR PFAM; PF00047; 19; 1.  
 FT NON\_TER 1 1  
 FT SEQUENCE 109 109 11646 MW; 5F675C52EC7EE197 CRC64;  
 SQ

Query Match 28.1%; Score 370; DB 4; Length 109;  
 Best Local Similarity 62.8%; Pred. No. 1.9e-25;  
 Matches 71; Conservative 22; Mismatches 14; Indels 6; Gaps 2;  
 OY 138 DIELTOSPSLAVSAGEKVMKSSOSLFSNRKRYLAWYQKQKQSPKLYIWASTR 197  
 DB 1 EYLVESGAEVKKPGASVSKASGYTFSSYYIMHWVROAPGGGLEMGIIINSGSTSY 55  
 OY 198 EGVGPRFTGSGSGDTFTLTISVQAEDLAVYCKOSYNLPTFGGKLEIK 249  
 DB 56 AFGIPDRFSGSGSGDTFTLTISRLPEDECAVYCCQYSSPLTFGGKVEIK 108

RESULT 8  
 O9UL74 PRELIMINARY; PRT; 99 AA.  
 AC 09UL74;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)  
 DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=Balb/C;  
 RA Maltiel S., Liao L., Cunningham M.W., Diamond B.;  
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-  
 acetyl-glucosamine antibodies from mice with autoimmune myocarditis".  
 RT Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF206032; AAF69330.1; -.  
 FT NON\_TER 1 1  
 FT SEQUENCE 99 99



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALE/C;  
 RA Maltiel S., Liao L., Cunningham M.W., Diamond B.;  
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-  
 acetyl-glucosamine antibodies from mice with autoimmune myocarditis."  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF206025; AAF69323.1; -  
 FT NON\_TER 1 114 1  
 FT 114 114  
 SQ SEQUENCE 114 AA; 12829 MW; 40485FDE6BA56F8 CRC64;

Query Match 27.9%; Score 367; DB 11; Length 114;  
 Best Local Similarity 61.1%; Pred. No. 3.7e-25;  
 Matches 69; Conservative 12; Mismatches 32; Indels 0; Gaps 0;

OY 10 ELVRSASVNLSTAGFINKDYMHVWVQREPEGLWIGYIDPESGEFEYAPNFGKAT 69  
 DB 2 QLVKPGASVKSCKASGYSTSYMHVWVQREPEGLWIGYIDPESGEFEYAPNFGKAT 61  
 OY 70 VYADISSNAYLHLSLSTEDTVVYCNVYVYEDYDALDYWGQGTAVVSS 122  
 DB 62 LTVKSSSTAYVQLSSPTSEDSAVYCCARSNYGSSLYYEDYWGQGTAVVSS 114

RESULT 13  
 ID 09UL77 PRELIMINARY; PRT; 108 AA.  
 AC 09UL77;

DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus."  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035037; AAD56273.1; -  
 DR HSSP; P01607; 1RET.  
 DR INTERPRO: IPR003006; -  
 DR PFAM; PF00047; 19; 1.  
 FT NON\_TER 1 108 1  
 FT 108 108  
 SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 27.8%; Score 365.5; DB 4; Length 108;  
 Best Local Similarity 61.9%; Pred. No. 4.6e-25;  
 Matches 70; Conservative 21; Mismatches 15; Indels 7; Gaps 2;

OY 138 DIELTOSPSLWASAGEKAMSKSSOSLFNSRTRKNYLAWYQKPGSKVLIYASTR 197  
 DB 1 DIOMTOSPSLSASVSGKRYITICRASOSI-----SYLAWYQKPGKAPNLIYASSL 54  
 OY 198 ESGVPRFTGSGSGDTFTLTSSVQAEDLAVYCKOSYNL-PTFGGKYLEIK 249  
 DB 55 QSGVPRFSGSGGDTFTLTSSVQAEDLAVYCKOSYNSWTFGGKYLEIK 107

RESULT 14  
 ID 09UL79

ID 09UL79 PRELIMINARY; PRT; 108 AA.  
 AC 09UL79;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus."  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035035; AAD56271.1; -  
 DR HSSP; P01607; 1RET.  
 DR INTERPRO: IPR003006; -  
 DR PFAM; PF00047; 19; 1.  
 FT NON\_TER 1 108 1  
 FT 108 108  
 SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 27.6%; Score 363.5; DB 4; Length 108;  
 Best Local Similarity 61.9%; Pred. No. 7e-25;  
 Matches 70; Conservative 19; Mismatches 17; Indels 7; Gaps 2;

OY 138 DIELTOSPSLWASAGEKAMSKSSOSLFNSRTRKNYLAWYQKPGSKVLIYASTR 197  
 DB 1 DIOMTOSPSLSASVSGKRYITICRASOSI-----SYLAWYQKPGKAPNLIYASSL 54  
 OY 198 ESGVPRFTGSGSGDTFTLTSSVQAEDLAVYCKOSYNL-PTFGGKYLEIK 249  
 DB 55 QSGVPRFSGSGGDTFTLTSSVQAEDLAVYCKOSYNSWTFGGKYLEIK 107

RESULT 15  
 ID 09UL75 PRELIMINARY; PRT; 109 AA.  
 AC 09UL75;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALE/C;  
 RA Maltiel S., Liao L., Cunningham M.W., Diamond B.;  
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-  
 acetyl-glucosamine antibodies from mice with autoimmune myocarditis."  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF206031; AAF69329.1; -  
 FT NON\_TER 1 109 1  
 FT 109 109  
 SQ SEQUENCE 109 AA; 12118 MW; FF65E4A1BBF936A6 CRC64;

Query Match 27.3%; Score 359; DB 11; Length 109;  
 Best Local Similarity 59.8%; Pred. No. 1.8e-24;  
 Matches 70; Conservative 16; Mismatches 19; Indels 12; Gaps 3;

OY 10 ELVRSASVNLSTAGFINKDYMHVWVQREPEGLWIGYIDPESGEFEYAPNFGKAT 69  
 DB 1 ELVKGASVKSCKASGYSTSYMHVWVQREPEGLWIGYIDPESGEFEYAPNFGKAT 60

Tue Feb 20 06:37:16 2001

us-09-297-181-4.rspt

Page 6

```
Qy      70 VTADTSNTAYLHLSLTSEPTVYVC-----NAVITYEIDGIALDYMGQGTIVVSS    122
        :|:| |:||: ||||||: ||| | | | | |||||:|||
Db      61 LTSDKSSSTAYMEISSLTSEDNAVYYCARDGN-----YRGF--DYMGGQTLLTVSS    109
```

```
Search completed: February 12, 2001, 15:24:31
Job time: 101 sec
```

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2001, 15:25:01 ; Search time 26.51 seconds

(without alignments)  
637.769 Million cell updates/sec

Title: US-09-297-181-4

Perfect score: 1315

Sequence: 1 QVKLOESGALVRSASVNL.....YKOSYNLPFGGKTLEIK 249

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	857	65.2	268	A56446	Ig heavy chain V r
2	854.5	65.0	249	S41374	single chain Fv an
3	841.5	64.0	233	JC3322	p53 specific singl
4	544	41.4	112	S43103	Ig kappa chain V-J
5	538	40.9	113	PT0407	Ig light chain V r
6	533	40.5	112	PL0265	Ig kappa chain V r
7	533	40.5	133	PS0023	Ig kappa chain pre
8	520	39.5	113	PT0408	Ig light chain V r
9	514	39.1	112	S41393	Ig kappa chain V r
10	503.5	38.3	111	S03304	Ig heavy chain V r
11	501.5	38.1	136	S04576	Ig heavy chain pre
12	498	37.9	104	PH1101	Ig light chain V r
13	497	37.8	103	PH1047	Ig light chain V r
14	497	37.8	104	PH1102	Ig light chain V r
15	492	37.4	103	PH1051	Ig light chain V r
16	492	37.4	103	PH1052	Ig light chain V r
17	492	37.4	104	PH1104	Ig light chain V r
18	491	37.3	103	PH1050	Ig light chain V r
19	489.5	37.2	220	A31790	Ig kappa chain V r
20	489	37.2	120	G33932	Ig kappa chain pre
21	486	37.0	135	S38807	Ig light chain V r
22	486	37.0	178	S29594	Ig gamma chain V-J
23	484.5	36.8	113	PL0263	Ig gamma chain (WM
24	484	36.8	101	PH1046	Ig kappa chain V r
25	484	36.8	104	PH1103	Ig light chain V r
26	480	36.5	111	G30502	Ig light chain V r
27	479	36.4	118	PT0356	Ig kappa chain V r
28	478.5	36.4	134	PC1214	Ig kappa chain pre
29	477.5	36.3	117	S17586	Ig heavy chain V r

30	477.5	36.3	214	2	S68212	Ig kappa chain (Ma
31	475	36.1	138	2	S26040	Ig kappa chain pre
32	474.5	36.1	113	2	PL0264	Ig kappa chain V r
33	474.5	36.1	120	2	S03471	Ig heavy chain V-D
34	470.5	35.9	240	2	S06084	Ig kappa chain pre
35	469	35.7	122	2	S06823	Ig heavy chain V r
36	468.5	35.6	112	2	E30538	Ig kappa chain V r
37	468.5	35.5	112	2	F30538	Ig kappa chain V r
38	468	35.6	116	2	S15672	Ig heavy chain V r
39	467.5	35.6	113	2	JC2270	PL7-6 antibody lig
40	467.5	35.6	118	2	S25174	Ig heavy chain V r
41	467	35.5	221	2	S49220	Ig gamma-1 chain -
42	466	35.4	112	2	S09970	Ig kappa chain V-J
43	465	35.4	97	2	A42575	Ig kappa chain V r
44	464	35.3	133	1	K4HUJ1	Ig kappa chain pre
45	463.5	35.2	113	2	S30520	Ig kappa chain V r

## ALIGNMENTS

RESULT 1  
A56446  
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996  
C:Accession: A56446  
R:Rang, P.M.; Polte, L.A.; Mahoney, W.C.; Schueler, P.A.  
J. Biol. Chem. 270: 7829-7835, 1995  
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally ide  
A:Reference number: A56446; MUID:95229583  
A:Accession: A56446  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-268 <TAN>  
A:Cross-references: CB:U20617  
C:Keywords: heterotrimer; immunoglobulin

Query Match 65.2%; Score 857; DB 2; Length 268;

Best Local Similarity 66.8%; Pred. No. 3.1e-54;  
Matches 167; Conservative 26; Mismatches 45; Indels 12; Gaps 3;

QY 1 QVKLOESGALVRSASVNLCTAGFNKDYMMHWKORPEGLWITGIDPESGETEY 60  
DB 3 QVKLOESGALVRSASVNLCTAGFNKDYMMHWKORPEGLWITGIDPESGETEY 62  
QY 61 APNFOGKATVTDTSNTAYLHLSLTSEDTVYVCNAVYYEYDGYALDWGQGTVTYV 120  
DB 63 DKPFOGKATVTDTSNTAYLHLSLTSEDTVYVCNAVYYEYDGYALDWGQGTVTYV 118  
QY 121 SSGGGSGGGGSGGGGSDIELTQSPSLAVSAGEVYAMSCAKSOSLFSRTKNTLAWQ 180  
DB 119 SSGGGSGGGGSGGGGSDIELTQSPSLAVSAGEVYAMSCAKSOSLFSRTKNTLAWQ 171  
QY 181 OKPGOSPVLITWASTRESGVDPRTSGSGGTDFTLITISVVAEDLAVYYCKOSYNLP-T 239  
DB 172 OKSDSPKLVITWASTRESGVDPRTSGSGGTDFTLITISVVAEDLAVYYCKOSYNLP-T 231  
QY 240 FGGGKTLEIK 249  
DB 232 FGGGKTLEIK 241

## RESULT 2

S41374  
single chain Fv antibody - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C:Accession: S41374  
R:Aitsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.  
submitted to the EMBL Data Library, January 1994  
A:Description: Construction and functional characterization of a single chain Fv anti





J. Exp. Med. 171, 265-297, 1990  
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
 A:Reference number: P10231; MUID:90111618  
 A:Accession: P10265  
 A:Molecule type: mRNA  
 A:Residues: 1-112 <SHL>  
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-23/Region: framework 1  
 F:16-96/Domain: immunoglobulin homology <IMM>  
 F:24-40/Region: complementarity-determining 1  
 F:41-55/Region: framework 2  
 F:56-62/Region: complementarity-determining 2  
 F:63-94/Region: framework 3  
 F:95-102/Region: complementarity-determining 3  
 F:103-112/Region: framework 4

Query Match 40.5%; Score 533; DB 2; Length 112;  
 Best Local Similarity 92.0%; Pred. No. 1.4e-31;  
 Matches 103; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 138 DIELTSPSSSLAVSAGEKYAMCKSSQSLFNSRTRKNYLAAYQKQSPKLIYASTR 197  
 ||:|||||  
 Db 1 DIYMSQSPSSSLAVSAGEKYAMCKSSQSLFNSRTRKNYLAAYQKQSPKLIYASTR 60

QY 198 ESGVPRFTGSGGTDFTLTISVQAEDLAAYYCKOSYNLPFGGKTLEIK 249  
 ||:|||||  
 Db 61 ESGVPRFTGSGGTDFTLTISVQAEDLAAYYCKOSYNLPFGGKTLEIK 112

RESULT 7  
 Ig kappa chain precursor V region (6A4) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 21-Jan-2000  
 C:Accession: PS00023  
 R:Margaret, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.  
 Gene 74, 335-345, 1988  
 A:Title: Cloning and characterization of cDNAs coding for the heavy and light chains of  
 A:Reference number: PS00023; MUID:89232725  
 A:Accession: PS00023  
 A:Molecule type: mRNA  
 A:Residues: 1-133 <MAR>  
 A:Experimental source: strain BALB/c  
 A:Note: the amino-terminal four residues of the mature protein were directly sequenced  
 C:Comment: This chain was obtained from a monoclonal antibody against Pseudomonas aerugi  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-133/Product: ig kappa chain V region 6A4 #status experimental <IGV>  
 F:36-116/Domain: immunoglobulin homology <IMM>

Query Match 40.5%; Score 533; DB 2; Length 133;  
 Best Local Similarity 89.7%; Pred. No. 1.7e-31;  
 Matches 104; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 134 GGGSDIELTSPSSSLAVSAGEKYAMCKSSQSLFNSRTRKNYLAAYQKQSPKLIYASTR 193  
 ||:|||||  
 Db 17 GTCGDIYMSQSPSSSLAVSAGEKYAMCKSSQSLFNSRTRKNYLAAYQKQSPKLIYASTR 76

QY 194 ASTRESGVPRFTGSGGTDFTLTISVQAEDLAAYYCKOSYNLPFGGKTLEIK 249  
 ||:|||||  
 Db 77 ASTRESGVPRFTGSGGTDFTLTISVQAEDLAAYYCKOSYNLPFGGKTLEIK 132

RESULT 8  
 Ig light chain V region (S107/VH11 group 1-6) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
 C:Accession: PT0408

R. Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharif, M.D.  
 J. Exp. Med. 173, 731-741, 1991  
 A:Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantib  
 A:Reference number: P10376; MUID:91147903  
 A:Accession: PT0408  
 A:Molecule type: DNA  
 A:Residues: 1-113 <BEH>  
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 39.5%; Score 520; DB 2; Length 113;  
 Best Local Similarity 90.2%; Pred. No. 1.2e-30;  
 Matches 101; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 138 DIELTSPSSSLAVSAGEKYAMCKSSQSLFNSRTRKNYLAAYQKQSPKLIYASTR 197  
 ||:|||||  
 Db 1 DIYMSQSPSSSLAVSAGEKYAMCKSSQSLFNSRTRKNYLAAYQKQSPKLIYASTR 60

QY 198 ESGVPRFTGSGGTDFTLTISVQAEDLAAYYCKOSYNLPFGGKTLEIK 249  
 ||:|||||  
 Db 61 ESGVPRFTGSGGTDFTLTISVQAEDLAAYYCKOSYNLPFGGKTLEIK 112

RESULT 9  
 Ig kappa chain V region (12.5H VL) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C:Accession: S41393  
 R:Margaret, C.; Gilbert, D.; Brard, F.; Tron, F.  
 submitted to the EMBL Data Library, January 1994  
 A:Description: Structural characterization of an (NZB x NZW)F1 mouse-derived Igm anti  
 A:Reference number: S41393  
 A:Accession: S41393  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-112 <MAR>  
 A:Cross-references: EMBL:229536  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 39.1%; Score 514; DB 2; Length 112;  
 Best Local Similarity 88.4%; Pred. No. 3.1e-30;  
 Matches 99; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 138 DIELTSPSSSLAVSAGEKYAMCKSSQSLFNSRTRKNYLAAYQKQSPKLIYASTR 197  
 ||:|||||  
 Db 1 DIYMSQSPSSSLAVSAGEKYAMCKSSQSLFNSRTRKNYLAAYQKQSPKLIYASTR 60

QY 198 ESGVPRFTGSGGTDFTLTISVQAEDLAAYYCKOSYNLPFGGKTLEIK 249  
 ||:|||||  
 Db 61 DSGVPRFTGSGGTDFTLTISVQAEDLAAYYCKOSYNLPFGGKTLEIK 112

RESULT 10  
 S03304  
 Ig kappa chain V region (61B8) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 21-Jan-2000  
 C:Accession: S03304; JI0043  
 R:Van Cleave, V.H.; Naeye, C.W.; Metzger, D.W.  
 J. Exp. Med. 167, 1841-1848, 1988  
 A:Title: Do antibodies recognize amino acid side chains of protein antigens indepen  
 A:Reference number: JI0043; MUID:88258372  
 A:Accession: S03304  
 A:Molecule type: mRNA  
 A:Residues: 1-111 <VAN>  
 A:Cross-references: EMBL:X12380; NID:952341; PIDN:CAA30938.1; PID:9930189  
 A:Note: the authors translated the codon GAT for residue 76 as Asn





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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2001, 15:26:39 ; Search time 16.14 Seconds

(without alignments)  
498.217 Million cell updates/sec

Title: US-09-297-181-4

Perfect score: 1315  
Sequence: 1 QVRLQESGAEIVRSGASVNL.....YCKQSYNLPFGGGRLEIK 249

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	464	35.3	133	KVAB_HUMAN	P06133 homo sapien
2	463.5	35.2	134	KVAC_HUMAN	P06125 homo sapien
3	448.5	34.1	114	KVAA_HUMAN	P06132 homo sapien
4	418	31.8	121	KV40_HUMAN	P01751 mus musculu
5	400	30.4	139	HV07_MOUSE	P01632 mus musculu
6	393.5	29.9	114	KVIA_MOUSE	P01745 mus musculu
7	393.5	28.9	120	HV03_MOUSE	P01633 mus musculu
8	380.5	28.9	149	KV5A_MOUSE	P01634 mus musculu
9	378.5	28.8	136	KV5B_MOUSE	P01755 mus musculu
10	378	28.7	137	HV11_MOUSE	P01746 mus musculu
11	376.5	28.6	140	HV02_MOUSE	P01745 mus musculu
12	373.5	28.6	121	HV01_MOUSE	P01745 mus musculu
13	371.5	28.3	129	KVIM_HUMAN	P04431 homo sapien
14	369.5	28.1	108	KVIM_HUMAN	P01600 homo sapien
15	367.5	27.9	108	HVIC_HUMAN	P01744 homo sapien
16	366	27.8	143	KV1C_HUMAN	P80362 homo sapien
17	365.5	27.8	108	KV1Y_HUMAN	P01664 mus musculu
18	363.5	27.8	111	KV3L_MOUSE	P01756 mus musculu
19	363.5	27.8	117	HV12_MOUSE	P01624 homo sapien
20	363	27.6	109	KV3F_HUMAN	P18135 homo sapien
21	362	27.5	129	KV3L_HUMAN	P01670 mus musculu
22	361.5	27.5	108	KV1V_HUMAN	P01670 mus musculu
23	361.5	27.5	111	KV3R_MOUSE	P01620 mus musculu
24	361	27.5	109	KV3B_HUMAN	P01622 homo sapien
25	361	27.5	109	KV3D_HUMAN	P01631 mus musculu
26	361	27.5	113	KV2G_MOUSE	P06309 mus musculu
27	360	27.4	117	KV3E_HUMAN	P01757 mus musculu
28	359.5	27.3	117	HV13_MOUSE	P06329 mus musculu
29	359	27.3	120	HV50_MOUSE	P04207 mus musculu
30	358.5	27.3	111	KV30_MOUSE	P04207 mus musculu
31	357	27.1	129	KV3M_HUMAN	P18136 homo sapien
32	357	27.1	129	KV3M_HUMAN	P01614 homo sapien
33	356.5	27.1	115	KV2A_HUMAN	P01614 homo sapien

34	355	27.0	108	1	KV3A_HUMAN	P01619 homo sapien
35	354.5	27.0	111	1	KV3T_MOUSE	P01672 mus musculu
36	354.5	27.0	138	1	HV48_MOUSE	P03980 mus musculu
37	354	26.9	107	1	KV1D_HUMAN	P01596 homo sapien
38	354	26.9	110	1	KV3P_MOUSE	P01668 mus musculu
39	353.5	26.9	111	1	KV3S_MOUSE	P01671 mus musculu
40	353	26.8	118	1	HV51_MOUSE	P06330 mus musculu
41	352.5	26.8	108	1	KV1P_HUMAN	P01608 homo sapien
42	352.5	26.8	108	1	KV5P_MOUSE	P01649 mus musculu
43	352.5	26.8	111	1	KV3Q_MOUSE	P01667 mus musculu
44	352	26.8	109	1	KV3E_HUMAN	P01623 homo sapien
45	352	26.8	113	1	KV2D_HUMAN	P01617 homo sapien

## ALIGNMENTS

RESULT	ID	QUERY	STANDARD	PRT	133 AA
1	KVAB_HUMAN				
AC	P06133:				
DT	01-JAN-1988 (Rel: 06, Created)				
DT	01-JAN-1988 (Rel: 06, Last sequence update)				
DT	15-JUL-1999 (Rel: 38, Last annotation update)				
DE	IG KAPPA CHAIN V-IV REGION JI PRECURSOR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE=86041853; PubMed=2997712;				
RA	Klobeck H.G., Bojnacki G.W., Combrato G., Mocikat R., Pohlentz H.D.,				
RT	Zachau H.G.;				
RT	"Subgroup IV of human immunoglobulin K light chains is encoded by a				
RT	single germline gene."				
RL	Nucleic Acids Res. 13:6515-6529(1985).				
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (see <a href="http://www.isb.ch/announce/">http://www.isb.ch/announce/</a>				
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
DR	EMBL: 200022; CAA77317.1; -				
DR	PIR: A01904; K450J1.				
DR	HSSP: P01789; 2MCP.				
DR	INTERPRO: IPR003006; -				
DR	PFAM: PF00047; Ig: 1.				
KW	Immunoglobulin V region; Signal.				
FT	SIGNAL	21	133		
FT	CHAIN	1	20		
FT	DOMAIN	21	43		
FT	DOMAIN	44	60		
FT	DOMAIN	61	75		
FT	DOMAIN	76	82		
FT	DOMAIN	83	114		
FT	DOMAIN	115	122		
FT	DOMAIN	123	132		
FT	DISULFID	43	114		
FT	NON_TER	133	133		
SQ	SEQUENCE	133 AA: 14632 MW: 5FB3953066744AF4 CRC64:			

Query Match: 35.3%; Score 464; DB 1; Length 133;  
Best local Similarity 75.0%; Pred. No. 1.2e-27;  
Matches 87; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 134 GGGSDELTFQSPSSLAIVSGEYVANSCKSSQSLNSRTKNTIATYQKPGGSPKYLTIW 193  
DB 17 GAYGDIWMTQSPDSLAIVSGERATINCKSSQSVLSSNNKNTIATYQKPGGPFLTIW 76

OY 194 ASTRESGVDPDRFTSGSGGDTFTLTSSVQAEDLAVYYCKOSYNLPFGGGTKLEIK 249  
 DB 77 ASTRESGVDPDRFTSGSGGDTFTLTSSVQAEDLAVYYCKOQYDTPFGGGTKVEIK 132

## RESULT 2

KV4C\_HUMAN STANDARD; PRT; 134 AA.

AC P06314;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-IV REGION B17 PRECURSOR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE-86041854; PubMed-2997713;  
 RA Marsh P., Mills F., Gould R.;

RT "Detection of a unique human V kappa IV germline gene by a cloned  
 RT cDNA probe."

RL Nucleic Acids Res. 13:6531-6544(1985).  
 RN [2]

RP REVISION TO 76.  
 RA Marsh P.;

RL Submitted (OCT-1986) to the EMBL/Genbank/DBJ databases.

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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC EMBL: X02990; CAA26733.1; -  
 DR PIR: A01905; K4H017.  
 DR HSSP: P01789; 2MCP.  
 DR INTERPRO: IPR003006; -  
 DR PFAM: PF00047; 19; 1.  
 DR KW Immunoglobulin V region; Signal.

CC FT CHAIN 1  
 CC FT SIGNAL 20  
 CC FT 1 134 IG KAPPA CHAIN V-IV REGION B17.  
 CC FT 21 134 FRAMEWORK 1.  
 CC FT 41 43 COMPLEMENTARITY-DETERMINING 1.  
 CC FT DOMAIN 44 60 FRAMEWORK 2.  
 CC FT 61 75 COMPLEMENTARITY-DETERMINING 2.  
 CC FT DOMAIN 76 82 FRAMEWORK 3.  
 CC FT 83 114 COMPLEMENTARITY-DETERMINING 3.  
 CC FT DOMAIN 115 121 FRAMEWORK 4.  
 CC FT 122 133 COMPLEMENTARITY-DETERMINING 4.  
 CC FT DOMAIN 134 134 BY SIMILARITY.  
 CC FT DISULFID 43 114  
 CC FT NON TER 134  
 CC FT 134 AA. 14966 MW; 6413A22FDD736832 CRC64;

SO SEQUENCE 134 AA. 14966 MW; 6413A22FDD736832 CRC64;

Query Match 35.2%; Score 463.5; DB 1; Length 134;  
 Best Local Similarity 76.1%; Pred. No. 1.3e-27;

Matches 89; Conservative 11; Mismatches 16; Indels 1; Gaps 1;

OY 134 GGSQDIETLQSPSSSLAVSAGEKYAMCKSSQSLFNSRTKNTIATYQKRGSPKLYIYW 193  
 DB 17 GAYGDIVMTQSPSLAVSLGERATINCKSSQSLVSSDNKNYLAWYQKRGSPKLYIYW 76

OY 194 ASTRESGVDPDRFTSGSGGDTFTLTSSVQAEDLAVYYCKOSYNLP-TFGGGTKLEIK 249  
 DB 77 ASTRESGVDPDRFTSGSGGDTFTLTSSVQAEDLAVYYCOQYDTPFGGGTKVEIK 133

## RESULT 3

KV4A\_HUMAN STANDARD; PRT; 114 AA.

ID KV4A\_HUMAN  
 AC P01625;

DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-IV REGION LEN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE-76004342; PubMed-50995;  
 RA Schneider M., Hilschmann N.;

RT "The primary structure of a monoclonic immunoglobulin-L-chain of  
 RT subgroup IV of the kappa type (Bence-Jones protein Len.)."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).  
 RN [2]

RP REVISION TO 9.  
 RA Salomon A.;

RL Submitted (AUG-1996) to the SWISS-PROT data bank.  
 CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC PIR: A01903; K4H01N.  
 DR HSSP: P01789; 2MCP.  
 DR INTERPRO: IPR003006; -  
 DR PFAM: PF00047; 19; 1.  
 DR KW Immunoglobulin V region; Bence-Jones protein.

CC FT CHAIN 1  
 CC FT DOMAIN 1 23 FRAMEWORK 1.  
 CC FT 24 40 COMPLEMENTARITY-DETERMINING 1.  
 CC FT DOMAIN 41 55 FRAMEWORK 2.  
 CC FT 56 62 COMPLEMENTARITY-DETERMINING 2.  
 CC FT DOMAIN 63 94 FRAMEWORK 3.  
 CC FT 95 101 COMPLEMENTARITY-DETERMINING 3.  
 CC FT DOMAIN 102 113 FRAMEWORK 4.  
 CC FT DISULFID 23 94 BY SIMILARITY.  
 CC FT NON TER 114  
 CC FT 114 AA. 12640 MW; 0647F1D1FE236485 CRC64;

SO SEQUENCE 114 AA. 12640 MW; 0647F1D1FE236485 CRC64;

Query Match 34.1%; Score 448.5; DB 1; Length 114;  
 Best Local Similarity 76.1%; Pred. No. 1.4e-26;

Matches 86; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

OY 138 DIELQSPSSSLAVSAGEKYAMCKSSQSLFNSRTKNTIATYQKRGSPKLYIYMASTR 197  
 DB 1 DIVMTQSPSLAVSLGERATINCKSSQSLVSSDNKNYLAWYQKRGSPKLYIYMASTR 60

OY 198 ESGVDPDRFTSGSGGDTFTLTSSVQAEDLAVYYCKOSYNLP-TFGGGTKLEIK 249  
 DB 61 ESGVDPDRFTSGSGGDTFTLTSSVQAEDLAVYYCOQYDTPFGGGTKLEIK 113

RESULT 4  
 KV4O\_HUMAN STANDARD; PRT; 121 AA.

AC P06312;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-IV REGION PRECURSOR (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE-86041853; PubMed-2997712;  
 RA Klobbeck H.G., Bornkamm G.W., Combiato G., Mocikat R., Pohlenz H.D.,  
 RA Zachau H.G.;

RT "Subgroup IV of human immunoglobulin K light chains is encoded by a  
 RT single germline gene."

RL Nucleic Acids Res. 13:6515-6529(1985).  
 CC -I- MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.

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ID KV5B_MOUSE STANDARD; PRT; 136 AA.
AC P01634;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-V REGION MOPC 21 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82059477; PubMed=6170937;
RA Hamlyn P.H., Galt M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming
and the diexonucleotide method of RNA sequencing.";
RL Nucleic Acids Res. 9:4485-4494(1981).
RN [2]
RP SEQUENCE OF 30-136.
RX MEDLINE=73053310; PubMed=4638343;
RA Swasti J., Milstein C.;
RT "The complete amino acid sequence of a mouse kappa light chain.";
RL Biochem. J. 128:427-444(1972).
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or send an email to license@isb-sib.ch).
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DR EMBL; V00810; CAA24192.1; ALT_TERM.
DR PIR; A01917; KYMS21.
DR INTERPRO; IPR003006;
DR PFAM; PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 29
FT CHAIN 30 136 IG KAPPA CHAIN V-V REGION MOPC 21.
FT DOMAIN 30 52 FRAMEWORK 1.
FT DOMAIN 53 63 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 64 78 FRAMEWORK 2.
FT DOMAIN 79 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 126 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 127 136 FRAMEWORK 4.
FT NON_TER 136
SQ SEQUENCE 136 AA; 14902 MW; 8CDD85113996D1C2 CRC64;

Query Match 28.8%; Score 378.5; DB 1; Length 136;
Best Local Similarity 63.2%; Pred. No. 2.2e-21;
Matches 74; Conservative 18; Mismatches 18; Indels 7; Gaps 2;

QY 134 GGGSDIELTSPSSLAIVASAGEKVMKSSQSLFNSTRKRYLAWYQKQSGSPKVLIV 193
DB 26 GAGNIVMTGSPKSMSSVGEVRLTLCKASENVY-----TYSWYQKPEQSPKLIIV 79

QY 194 ASTRESGVPRFTGSGGSDFTLTISVQAEADLAIVYCKKSYNLP-TFGGKTLEIK 249
DB 80 ASNRKTVGPDRFTGSGGSDFTLTISVQAEADLAIVYCKKSYNLP-TFGGKTLEIK 136

RESULT 10
HVL1_MOUSE STANDARD; PRT; 137 AA.
ID HVL1_MOUSE
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00539; AAA38172.1;
DR PIR; A02038; G2MS43.
DR INTERPRO; IPR003006;
DR PFAM; PF00047; 15; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 FRAMEWORK 3.
FT DOMAIN 86 117 FRAMEWORK 4.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8BC9 CRC64;

Query Match 28.7%; Score 378; DB 1; Length 137;
Best Local Similarity 61.5%; Pred. No. 2.4e-21;
Matches 75; Conservative 11; Mismatches 32; Indels 4; Gaps 2;

QY 1 0VKLOSAGELVSGASVYNLCSTASGFNIDYMHVWKPREGSLWIGIDPESGTEY 60
DB 20 QVDDQPGAEVPGASVSKSCASGTTFTSYLHMVWNPGRGLEIGIDNSGCTTY 79

QY 61 APNPGKATVYADTSNTAVILHLSLTSEDTVYCNNAVITYEYDGYALDYGOGTTVY 120
DB 80 NEHFRSKATITIDKPSSTAVMQLSSLSSEDSAVYYC---ARYRLGRY-PDYWGOGTTLTY 135

QY 121 SS 122
DB 136 SS 137

RESULT 11
HVL2_MOUSE STANDARD; PRT; 140 AA.
ID HVL2_MOUSE
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82152813; PubMed=6801765;
RA Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;

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"Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain."

RT Science 216:309-311(1982).  
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CC EMBL: J00493; AAA38128.1; -  
 DR PIR: A02028; HVM5G7.  
 DR INTERPRO: IPR003006; -  
 DR PFAM: PF00047; 19; 1.  
 KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.  
 FT NON\_TER 140 140  
 SQ SEQUENCE 140 AA; 15514 MW; 254ACBBE31DA5CE8 CRC64;

Query Match 28.6%; Score 376.5; DB 1; Length 140;  
 Best Local Similarity 58.2%; Pred. No. 3.1e-21;  
 Matches 71; Conservative 19; Mismatches 31; Indels 1; Gaps 1;

OY 1 OVLOESGAEIVRSAGVNSCTASGFNKKDYMHVKKORPEGLMEIGYIDPESGETEY 60  
 DB 20 EVLOQSGAEIVRSAGVNSCTASGFNKKDYMHVKKORPEGLMEIGYIDPESGETEY 79  
 OY 61 APNFOGKATYADTSSNTAYLHLSLTSEDTYYCNAVYYEYEDGALDYWGSGTYYTV 120  
 DB 80 NEKKKGATITLVDRSSSTAVWQLRSLSEDSAVYFCARSHYIG-GSYDPFDWGGTFLTV 138

OY 121 SS 122  
 DB 139 SS 140

RESULT 12  
 HVOI\_MOUSE  
 ID HVOI\_MOUSE STANDARD; PRT; 121 AA.

AC P01745;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V REGION MPC 11.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RP [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE-81053741; PubMed-6253904;  
 RA Zakut R., Cohen J., Givol D.;  
 RT Cloning and sequence of the cDNA corresponding to the variable  
 RT region of immunoglobulin heavy chain MPC11."  
 RL Nucleic Acids Res. 8:3591-3601(1980).

RP REVISIONS.  
 RA Zakut R., Cohen J., Givol D.;  
 RL Nucleic Acids Res. 8:4839-4840(1980).  
 CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED  
 CC FROM A MYELOMA THAT SECRETES IGG2B.  
 DR PIR: A02027; GYMS11.  
 DR INTERPRO: IPR003006; -  
 DR PFAM: PF00047; 19; 1.  
 KW Immunoglobulin V region.  
 FT NON\_TER 121 121  
 SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 28.6%; Score 375.5; DB 1; Length 121;

Best Local Similarity 59.0%; Pred. No. 3.2e-21;  
 Matches 72; Conservative 18; Mismatches 31; Indels 1; Gaps 1;

OY 1 OVLOESGAEIVRSAGVNSCTASGFNKKDYMHVKKORPEGLMEIGYIDPESGETEY 60  
 DB 1 EVLOQSGAEIVRSAGVNSCTASGFNKKDYMHVKKORPEGLMEIGYIDPESGETEY 60  
 OY 61 APNFOGKATYADTSSNTAYLHLSLTSEDTYYCNAVYYEYEDGALDYWGSGTYYTV 120  
 DB 61 NDNLKKGATITLVDRSSSTAVWQLRSLSEDSAVYFCARSHYIG-GSYDPFDWGGTFLTV 119

OY 121 SS 122  
 DB 120 SS 121

RESULT 13  
 KVIH\_HUMAN  
 ID KVIH\_HUMAN STANDARD; PRT; 129 AA.

AC P04431;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RP [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE-85014148; PubMed-6091049;  
 RA Klobbeck H.G., Combratio G., Zachau H.G.;  
 RT "Immunoglobulin genes of the kappa light chain type from two human  
 RT lymphoid cell lines are closely related."  
 RL Nucleic Acids Res. 12:6995-7006(1984).

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CC EMBL: X00965; CAA25477.1; ALT\_TERM.  
 DR PIR: A01883; KIH0WK.  
 DR HSSP: P01607; 1REI.  
 DR INTERPRO: IPR003006; -  
 DR PFAM: PF00047; 19; 1.  
 KW Immunoglobulin V region; Signal.

FT SIGNAL 1 22  
 FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.  
 FT DOMAIN 23 45 FRAMEWORK 1.  
 FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 57 71 FRAMEWORK 2.  
 FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 79 110 FRAMEWORK 3.  
 FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 120 129 FRAMEWORK 4.  
 FT DISULFID 45 110 BY SIMILARITY.  
 FT NON\_TER 129 129  
 SQ SEQUENCE 129 AA; 14069 MW; F941FA07DAFC2F9 CRC64;

Query Match 28.3%; Score 371.5; DB 1; Length 129;  
 Best Local Similarity 62.4%; Pred. No. 6.6e-21;  
 Matches 73; Conservative 20; Mismatches 17; Indels 7; Gaps 2;

OY 134 GGGSDIELTQSPSSSLAVSAGEKVMKCSKSSQSLFNSRTKKNYLAWYQKPGSKVLYTV 193  
 DB 19 GACDIDQMGSPSSSLAVSAGEKVMKCSKSSQSLFNSRTKKNYLAWYQKPGSKVLYTV 72  
 OY 194 ASTRESGVDPFTGSGGDTFTLTSSVOAEDLAVYCKQSTN-LPTFGCGKLEIK 249  
 DB 194 ASTRESGVDPFTGSGGDTFTLTSSVOAEDLAVYCKQSTN-LPTFGCGKLEIK 249

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DB 73 ASSLOGSVTSRFGSGSGDTFTLTISLQPEDSATYTCQGSYSTLTFTFGGTRELEIK 129
RESULT 14
KVIM_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION LAY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP MEDLINE-77038198; PubMed-824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IGM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities."
RL Scard J. Immunol. 5:677-684(1976).
CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
CC PIR: A01871; KIHUX.
CC HSSP: P01607; IREL.
DR HSSP; P01607; IREL.
DR INTERPRO: IPR003006;
DR PFAM: PF00047; 1g; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34 FRAMEWORK 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 89 97 FRAMEWORK 3.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 23 88 FRAMEWORK 4.
FT NON_TER 108 108 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 28.1%; Score 369.5; DB 1; Length 108;
Best Local Similarity 62.8%; Pred. No. 7.6e-21;
Matches 71; Conservative 20; Mismatches 15; Indels 7; Gaps 2;

QY 138 DIETQSPSSLAIVSAGEKVMSCSSQSLFNSRTRKNTLAWYQKPGQSPKVLIIYMASTR 197
DIETQSPSSLAIVSAGEKVMSCSSQSLFNSRTRKNTLAWYQKPGQSPKVLIIYMASTR 197
DB 1 DIETQSPSSLAIVSAGEKVMSCSSQSLFNSRTRKNTLAWYQKPGQSPKVLIIYMASTR 54
DIETQSPSSLAIVSAGEKVMSCSSQSLFNSRTRKNTLAWYQKPGQSPKVLIIYMASTR 54

QY 198 ESGVPRFTGSGSGDTFTLTISVQAEDLAVYCKOSYNL-PTFGGKLEIK 249
ESGVPRFTGSGSGDTFTLTISVQAEDLAVYCKOSYNL-PTFGGKLEIK 249
DB 55 EAGVPRFTGSGSGDTFTLTISVQAEDLAVYCKOSYNL-PTFGGKLEIK 107
EAGVPRFTGSGSGDTFTLTISVQAEDLAVYCKOSYNL-PTFGGKLEIK 107

RESULT 15
KVIM_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION HAU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP MEDLINE-71032830; PubMed-4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
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RT chain of subgroup I (Bence-Jones Protein HAU): subdivision within
RT subgroups.
RT Hoppe-Seidler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR: A01868; KIHOU.
CC HSSP: P80362; IWTL.
DR INTERPRO: IPR003006;
DR PFAM: PF00047; 1g; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 FRAMEWORK 2.
FT DOMAIN 35 49 FRAMEWORK 3.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 89 97 FRAMEWORK 3.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 23 88 FRAMEWORK 4.
FT NON_TER 108 108 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 27.9%; Score 367.5; DB 1; Length 108;
Best Local Similarity 61.9%; Pred. No. 1.1e-20;
Matches 70; Conservative 22; Mismatches 14; Indels 7; Gaps 2;

QY 138 DIETQSPSSLAIVSAGEKVMSCSSQSLFNSRTRKNTLAWYQKPGQSPKVLIIYMASTR 197
DIETQSPSSLAIVSAGEKVMSCSSQSLFNSRTRKNTLAWYQKPGQSPKVLIIYMASTR 197
DB 1 DIETQSPSSLAIVSAGEKVMSCSSQSLFNSRTRKNTLAWYQKPGQSPKVLIIYMASTR 54
DIETQSPSSLAIVSAGEKVMSCSSQSLFNSRTRKNTLAWYQKPGQSPKVLIIYMASTR 54

QY 198 ESGVPRFTGSGSGDTFTLTISVQAEDLAVYCKOSYNL-PTFGGKLEIK 249
ESGVPRFTGSGSGDTFTLTISVQAEDLAVYCKOSYNL-PTFGGKLEIK 249
DB 55 EAGVPRFTGSGSGDTFTLTISVQAEDLAVYCKOSYNL-PTFGGKLEIK 107
EAGVPRFTGSGSGDTFTLTISVQAEDLAVYCKOSYNL-PTFGGKLEIK 107
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